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Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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AAM79312	AAE13149	ABO4415	ABR62108	ABR62115	ABR58489	ADE07919	ABR62110	ABR62113	AAE13162	AB044426	AAB37115	ABG76508	ABR62106	AAB36166	ABR62101	ABR62107	ABR62102	ADB76146	AAB13155
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56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis; parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disease; parkinson's disease; alsoimune disease; autoimune disease; autoimune disease; autoimune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell. Drmanac RT; Liu C, Tillinghast JS, Sinku A, Liu C ckson M, Mize NK, Nishikawa M; Human stem cell growth factor-like protein #3. AAE13151 standard; protein; 273 AA 05-APR-2000; 2000US-00543174. 28-JUN-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757562. 05-PBB-2001; 2001US-0266614P. 35-APR-2001; 2001WO-US011208 Tang TY, Labat I, Tillingh Stache-Crain B, Dickson M, (first entry) (HYSB-) HYSBQ INC. (KIRI) KIRIN BEER KK. WPI; 2001-657166/75. N-PSDB; AAD21725. TO200177169-A2. Homo sapiena 28-JAN-2002 18-OCT-2001.

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow cell. The haematopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as a graft for the bone marrow cransplantation or cord blood transplantation for treating a variety of disease such as immunodeficiency syndrome, agammaglobulinaemia, whishort-Aldrich syndrome, agammaglobulinaemia, haemolytic anaemia deuce to enzyme defect, congenital anaemia such as sickle cell anaemia, Gaucher's disease, lysosomal storage diseases such as mucopolysactoharidosis, adrenal white matter categoneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiency syndrome deficiency syndrome deficiency syndrome deficiency accounting atthrible sclerosis, systemic continue describle and the immunodeficiency continued and such as multiple sclerosis, systemic continued and such as multiple sclerosis, systemic continued and such as manifical anaemia and autoimmune disorders such as multiple sclerosis, systemic continued and such as severe combined immunodeficiency and the such as multiple sclerosis, systemic continued and such as a such as and character and a severe combined immunodeficiency and the such as a such as and should a systemic combined and such as a such as 
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    cancer, rheumatoid arthritis, osteoporosis.
                                                                               Claim 28; Page 214-215; 232pp; English.
    disease,
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Sequence 273 AA;

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RLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFY 120
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Query Match 100.0%; Score 1516; DB 4; Length 273; Best Local Similarity 100.0%; Pred. No. 3.8e-111; Matches 273; Conservative 0; Mismatches 0; Indels 0.
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immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cell; wound healing; haematopoietic progenitor cell; stromal cell; AIDS, thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemla;
                                                                                                                                                                    cell growth factor-like protein; antianemic; anti-HIV; SCR-1;
                                                                                                                            Human stem cell growth factor-like protein, SCR 1 #2.
  ABO44414 standard; protein; 273 AA
                                                                                    (first entry)
                                          AB044414;
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congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.

Homo sapiens.

US2003044792-A1.

06-MAR-2003

28-JUN-2001; 2001US-00894912.

28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P.

TANG/)

DRMANAC R T. TANG Y T. LABAT I. LABA/

MIZE N. NISHIKAWA M. (DRMA/) (MIZE/) (NISH/)

CHAO C. CHAO/)

ΰ Chao Drmanac RT, Mize N, Nishikawa M, Labat I, rang YT,

WPI; 2003-625403/59. N-PSDB; ACH04325

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.

Claim 23; Page 72-73; 96pp; English.

The invention relates to an isolated stem cell growth factor-like collypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth carried carcivaty. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide, a host cell genetically engineered to contain the SCR-1 polymucleotide, a host cell genetically engineered to contain the SCR-1 polymucleotide in operative association with a requising the carpression product of the SCR-1 polymucleotide in the host cell, that controls expression of the SCR-1 polymeleotide in the host cell, that controls expression of the SCR-1 polymeleotide in the host cell, corresponding an expression of the SCR-1 polymeleotide with stem cell growth factor activity and activity to support proliferation or survival of haematopoletic stem cell acting any 10 consecutive as from Abo44430, an isolated SCR-1 polymeptide with stem cell growth factor activity and lacking any 10 consecutive and from Abo44430, an isolated strain and Abo44428 and Abo4 transplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia,

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Wiskott-Aldrich syndrome, AIDS, etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial enl growth, and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1
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100.0%; Pred. No. 3.8e-111;
ive 0; Mismatches 0;
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inflammation disease
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N-PSDB; AAH45131.
                                                                                                                                                                                        Local Similarity
                                                                                                                                         Sequence 273 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-1999;
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                                                                                                                                                                        Query Match
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                                                                                                              protein
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The present sequence is the protein sequence for human thrombospondin-30. Thrombospondin-30 protein and coding sequence are useful in the diagnosis and treatment of malignant thunour, hasemopathy, HIV infection, immunological diseases and various inflammation diseases. In addition
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                                                                                                                                                                                                                                                                                                                                                       62 PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGPYLH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                           122 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEMNPMSPCTKKGKTCGFKRGTETRVREIIQ 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; atem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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, Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKENKGESKEAI PDSKSLESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 HPSAKGNI,CPPTNETRKCTVQRKKCOKGERGKKGRERKRKKPNKGESKBAIPDSKSLESS
                                                                                                                                                                                                                                                                                   HIRLISWLFIILMFWEYIGSQNASRGRRQRRWHPNVSQGGCGATCSDYNGCLSCKPRL
                                                                                                                                                                                                                                                                                                                                      63 PPALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLH
                                                                                                                                                                                                                                                                                                                                                                                                         LGKCLDNCPEGLEANNHTMECVS I VHCEVSEWNPWS PCTKKGKTCGFKRGTETRVREI 1Q
                                                                thrombospondin-30 protein may be used for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The thrombospondin-30 coding sequence may be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or in producing gene chips or microarrays
                                                                                                                                                                                                                                                                      3 HIRLISWIFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                     Length 272;
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Wang D, Wang J, Zhang J, Ren F,
                                                                                                                                                                                              / Match 99.3%; Score 1505; DB 4; L Local Similarity 100.0%; Pred. No. 2.8e-110; nes 271; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 KEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRIPEQRENKOOOKKRKVODKOKSVSVSTVH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-2000; 2000US-00560875.
20-UTN-2000; 2000US-00590875.
19-UTL-2000; 2000US-0052325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-CCT-2000; 2000US-0063325.
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                                                                                                                                                                    Sequence 272 AA;
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Ma Y, Zhao QA,
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                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SRQ ID NO 2110 (AAK52581), 2111
                                                                   Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PFALERIGHKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKCRERKRKKPNKGESKEAIPDSKSLESS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; stem cell growth factor-like protein; antinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; Wiskott-Aldrich syndrome; AlDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzhekimer's disease; thromboryopeania; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                     2 HLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQCCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                                                                                                                                                                                                                                                                         3 HLRLISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
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                                                                                                                                                                                                                                                                                                                                                    Length 272;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                   Query Match
99.3%; Score 1505; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 2.8e-110;
Matches 271; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human stem cell growth factor-like protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEI PEORENKOOOKKRKVODKOKSVSVSTVH 273
 Goodrich R;
                                                                                                          Claim 20; Page 3214-3215; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE13168 standard; protein; 272 AA
 Yang Y, Wejhrman T,
                                                                                 in diagnosis and gene therapy
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                            2001-476283/51.
                                        N-PSDB; AAK51461
                                                                                                                                                                                                                                                                                                                            Sequence 272 AA;
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  Xue AJ,
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known solymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SKTH). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, haematopoietic progenitor cell, historially principal cell, haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The proteins can replace as a graft for the bone marrow factor-like proteins can replace as a graft for the bone marrow of disease, such as immunodeficiency syndrome, agammaglobulinaemia, disease, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), cuch as sickle cell anaemia, Gaucher's disease, lysosomal storage chiseases such as succhains diseases, lysosomal storage celseneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as severe combiocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLH 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel stem cell growth factor like polypeptides and polymucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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                                                                                                                                                                                                                                                                                                    22. .272 /note= "Human mature stem cell growth factor-like
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supporting factor for the proliferation of stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 28; Page 226-227; 232pp; English.
                                                                                                                                                                                                                      1. .21
/label= Signal_peptide
                                                                                                                                                                      ocation/Qualifiers
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09-JAN-2001; 2001US-00757562.
05-PEB-2001; 2001US-0266614P.
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Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                              protein"
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(KIRI ) KIRIN BEBR KK
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                                                                                                    Homo sapiens
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                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                             Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immune deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher; a disease; lysosomal storage disease; mccopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                          181
                                                                               242
LGKCLDNCPEGLEANNHTMECVSIVHCEVSERNPWSPCTKKGKTCGPKRGTETRVREIIQ 182
                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                183 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKKGRERKRKKPNKGESKEAIPDSKSLESS
                                                                                           22. .272 ____/note= "Human mature stem cell growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tillinghast JS, Sinku A, Liu C,
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Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
                                                                                                                                                                                                                                                                         Human stem cell growth factor-like protein #2
                                                                                                                                      242 KEIPEGRENKQQKKRKVQDKQKSVSVSTVH 272
                                                                                                                           243 KEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 273
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                       AAE13150 standard; protein; 272 AA
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2000US-0215733P.
2001US-00757562.
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N-PSDB; AAD21724.
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28-JUN-2000;
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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of seem cells (STCH-1). Stem cell growth factor-like proteins are useful for supporting proliferation or call growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell, embryonic stem cell, paramatopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth cactor-like proteins can replace as a graft for the bone marrow cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous (Miskott-Aldrich syndrome, acquired immune deficiency syndrome, sagammaglobulinaemia, wiskott-Aldrich syndrome, adultence immune deficiency syndrome, adultence, and such as micopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention care useful for treating diseases such as severe combined immunodeficiency of disease and other neurodegenerative diseases, thrombocyclopenia, immune deficiencies and disorders such as multiple sclerois, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequence is stem cell growth factor-like protein from human
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Claim 28; Page 211-212; 232pp; English.
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Matches 271; Conservative
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30-AUG-2002; 2002WO-US027746. 30-AUG-2001; 2001US-0316368P.

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The invention relates to new stem cell growth factor-like polypeptides and polymuclectides. The stem cell growth factor-like polypeptides and polymuclectides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerative diseases like Alzheimer's leukaemia, paemophilia and degeneratiny ediseases. They are also useful for generating new tissues and organs that may aid patients in need of transplanted tissues. The polymuclectides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in generating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed generating antibodies that specifically bind the polypeptide, as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current or prevention of cancers, and other immunological disorders. The current sequence represents a human clone 1 thrombospondin protein
                                                                                                                                                                                                                                                                                                  New stem cell growth factor-like polypeptides and polynucleotides, use for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Pig 1; 151pp; English
                                                                                                        10-DEC-2001; 2001US-0339739P.
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                                                                                                                                                                     (HYSE-) HYSEQ INC.
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63 PPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122 62 PFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLH 121 123 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKBAIPDSKSLESS 242 241 62 19 2 HLRLISWLFIILNFWBYIGSQNASRGRRQRRMHPNVSQGCQGGGATCSDYNGCLSCKPRL 182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKRAIPDSKSLESS HLRLISWLPIILNFWBYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPRL GapB ó Length 272; 0; Indels 99.3%; Score 1505; DB 6; L 100.0%; Pred. No. 2.8e-110; iive 0; Mismatches 0; 243 KRIPEORENKOOOKKRKVODKOKSVSVSTVH 273 Matches 271; Conservative Local Similarity 183 Query Match 셤 ሯ 셤 8 유 ŝ 음 ò

ABO44432 standard; protein; 272 AA ABO44432; ABO44432 ID ABO4 XX AC ABO4 XX DT 30-S RESULT 8

242 KEIPEGRENKOOOKKRKVODKOKSVSTVH 272

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30-SEP-2003 (first entry)

Human stem cell growth factor-like protein, SCR 1 #4.

Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian folliche development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.

Homo sapiens

22. .272 /notes "Mature stem cell growth factor-like protein. This protein is specifically claimed in claim 9" 1. .21 /label= Signal_peptide Location/Qualifiers Pept 1de Protein

US2003044792-A1

06-MAR-2003

28-JUN-2001; 2001US-00894912.

28-JUN-2000; 2000US-0215733P. 05-PEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P.

(TANG/) TANG Y T. (LABA/) LABAT I.

DRMANAC R T. (DRMA/)

MIZE N. NISHIKAWA M. CHINO C. (NISH/) (CHAO/) Chao C; Drmanac RT, Mize N, Nishikawa M, Tang YT, Labat I,

WPI; 2003-625403/59. N-PSDB; ACH04328 Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.

Claim 23; Page 82; 96pp; English.

The invention relates to an isolated stem cell growth factor-like colls (SCR-1) from mouse or human, or its mature protein portion, or cells (SCR-1) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polynucleotide encoding CC SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polynucleotide, an (expression) vector comprising the CC SCR-1 polynucleotide in operative association with a regulatory sequence CC SCR-1 polymucleotide in operative association with a regulatory sequence CC SCR-1 polymore of the polynucleotide in the host cell, corression product of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide having an extryity to support proliferation or survival of haematopoietic stem cell cC comprise the as sequence appearing as ABO44431, an isolated SCR-1 polypeptide with stem cell growth factor activity and cisolated SCR-1 polypeptide with stem cell growth factor activity and constrain as as from ABO44430, an isolated polypeptide (with stem cell growth factor activity having at least an as sequence appearing as ABO44428 and ABO44429, a culture medium comprising the SCR-1 polypeptide in promocupie product proliferation of a stem collypeptide to maintain survival of or promocup proliferation of a stem

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ccell or germ cell, an anti-SCR l antibody, a nucleic acid array

C comprising the SCR-1 polynucleotide or a unique segment of the SCR-1

C polynucleotide attached to a surface, a stronal cell genetically

c engineered to express the SCR-1 polypeptide to support proliferation or

Survival of a stem cell or germ cell and an implant comprising a cell

c genetically engineered to express the SCR-1 polypeptide to support

C proliferation or survival of a stem cell. The SCR-1

polypeptide is useful for identifying a compound that binds to the SCR-1

polypeptide and for maintaining survival of or promoting proliferation of

C progenitor cell. The SCR-1 polypeptide is useful for promoting wound

C progenitor cell. The SCR-1 polypeptide is useful for promoting wound

C progenitor cell culture using the SCR-1 plypeptide can replace as a

C progenitor cell culture using the SCR-1 plypeptide can replace as a

C progenitor cell culture using the SCR-1 plypeptide can replace as a

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C progenitor the conventional bone marrow transplantation or cord blood

C progenitor the conventional bone marrow transplantation or cord blood

C progenitor the conventional bone marrow transplantation or cord blood

C progenitor the conventional bone marrow transplantation cord blood

C progenitor the conventional bone marrow transplantation or cord blood

C progenitor cell culture using the SCR-1 polypeptide is useful for cell growth and

C due to enzyme defect. congenital anemia such as slicklaemia, daucher's

C morphogenesis, including tissue specific stem cell growth, and regulation, ovarian follicle development, promoting nerve

C properior and immunosuppression. The present sequence is a Human SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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Sequence 272 AA;

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242
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                                                                                                       2 HLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKFRL
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                                                                                  3 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
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99.3%; Score 1505; DB 6; Length 272;
100.0%; Pred. No. 2.8e-110;
ive 0; Mismatches 0; Indels (
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                       al Similarity 100.0%; Pred. No. 2.8 271; Conservative 0; Mismatches
                     Local Similarity
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Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; coaling; hone growth; immunosuppression; human.
                                                                                                                                                                        Human stem cell growth factor-like protein, SCR 1 #1.
                                          ABO44413 standard; protein; 272 AA
                                                                                                                                (first entry)
                                                                                                                                  30-SEP-2003
                                                                                       ABO44413;
RESULT 9
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c SCR-1 polymorlectide in the host cell, preparesion of the golymorlectide in the host cell, preparesion of the SCR-1 polymorlectide which is an expression product of the SCR-1 polymorlectide (the polypeptide having an activity to support proliferation or survival of haematopoietic stem cell cartivity to support proliferation or survival of haematopoietic stem cell cartivity to support proliferation or survival of haematopoietic stem cell conditions as ABO44431), an isolated SCR-1 polymorlectide with stem cell growth factor activity and isolated SCR-1 polypeptide with stem cell growth factor activity and lacking any 10 consecutive ass from ABO4430, an isolated polypeptide with stem cell growth factor activity and compraint as ABO44428 and ABO44429, a culture medium comprising the SCR-1 polymorlectide or a unique segment of the SCR-1 polymorlectide or a unique segment of the SCR-1 polymorlectide or a unique segment of the SCR-1 polymorlectide or surport proliferation or survival of a stem cell as surface, a stromal cell genetically comprising the SCR-1 polymorlectide or a unique segment of the SCR-1 polymorlectide or support proliferation or survival of a stem cell as surface, a stromal cell genetically component of a surface, a stromal cell genetically component or survival of a stem cell or gene cell or gene cell or genetically engineered to express the SCR-1 polymorlectide to support proliferation or survival of a stem cell or gene cell or genetically engineered to express the SCR-1 polymorlectice stem cell or a haematopoietic componenting survival of a stem cell or a haematopoietic component or cell component or cell or a haematopoietic component or cell or a haematopoietic component or cell or the conventional bone marrow transplantation or cell scan be comployed as a therapy for treating diseases such as chronic granulomators diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia when the conventional publicated or cell growth as sicklaemia due to enzyme defect, congenital su seeful for cell g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem feragement, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polynucheotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polynucleotide), an (expression) vector comprising the SCR-1 polynucleotide, a host cell genetically engineered to contain the SCR-1 polynucleotide in operative association with a regulatory sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor
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05-FEB-2001; 2001US-026614P.
05-APR-2001; 2001US-0282397P.
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morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuropyotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wishort-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis;
                                                                                                                                                                                                                                                                                                                                                                                      PPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQ 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson'e disease; Alzheimer's disease; thrombocytopenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune pulmonary inflammation, cancer, tumour, gene therapy, SCR-1, supporting factor for the proliferation of stem cell; secreted protein.
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                                                                                                                                                                                                                                                                                            3 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
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                                                                                                                                                                                                   Length 272;
                                                                                                                                                                                                   99.3%; Score 1505; DB 6; Length 2'
100.0%; Pred. No. 2.8e-110;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein from clone DA228_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE13163 standard; protein; 265 AA
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28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-PRB-2001; 2001US-0266614P.
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KIRIN BEER
                                                                                                                                                        Sequence 272 AA;
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Best Local S
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ID AAR13163
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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, emrenced for supporting proliferation or survival of a stem cell, embryonic stem cell, paramatopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth catorilke proteins can replace as a graft for the bone marrow transplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous of disease, duplicated immunodeficiency syndrome, chronic granulomatous wiskott-Aldrich syndrome, acquired immune deficiency syndrome, lubs), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia culs as sickle cell anaemia due to enzyme defect, congenital anaemia degeneration, a variety of cancer and tumours. Proteins of the invention care useful for traating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as multiple sclerosis, a disease, Alzheimer's clisease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune such as evere combined immune pulmonary inflammation. Sequence is human secreted protein from clone DA228_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
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                                                                                                                                                                                    Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ
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Drmanac RT;
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Sinku A, Liu C,
Tang TY, Labat I, Tillinghast JS, Sinku A, Liu Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
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Best Local Similarity 100.(
Matches 264; Conservative
                                                                                                             WPI; 2001-657166/75.
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The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem colls (SCR-1)) from mouse or human, or its mature protein portion, or call famure protein portion, or call famure protein portion, or call growth factor activity. Also included are an isolated polymuclectide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the scrivity and required stem cell growth factor activity, or the complement of the polymuclectide, a most cell genetically engineered to contain the SCR-1 polymuclectide, a polymptide in the host cell, preparation of the SCR-1 polymuclectide in the host cell, preparation of the SCR-1 polymuclectide in the host cell, that controls expression product of the SCR-1 polymuclectide in the host cell, carrivity to support proliferation or survival of hasmatopoietic stem cell cartivity to support proliferation or survival of hasmatopoietic stem cell cartivity to support proliferation or survival of hasmatopoietic stem cell cartivity having at least an as sequence does not comprise the as sequence appearing as ABO44433 and ABO44430, an sisolated SCR-1 polypeptide with stem cell growth factor activity having at least an as sequence comprising the SCR-1 polymuclectide to maintain survival of or promote proliferation or survival of a stem cell or gene cell or gene cell or gene cell or gene cell or spense the SCR-1 polymuclectide to support proliferation or survival of a stem cell or gene cell or stem cell and an implant comprising to onlypeptide and for maintaining survival of or promoting proliferation or survival or a stem c
Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; haemolytic anaemia; congenital anaemia; wishact-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sichlaemia; Guotheri's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.
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05-APR-2001; 2001US-0282397P.
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MIZE N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MIZE/)
(NISH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TANG/)
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healing. The human haematopoietic stem cell or human haematopoietic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, AIDS. etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a protein homologous to Human SCR-1 protein
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                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                               Length 265;
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                                                                                                                                                                                                                                                                            97.1%; Score 1472; DB 6; Length 2
100.0%; Pred. No. 1.1e-107;
ive 0; Mismatches 0; Indels
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Drmanac RT;

Labat I, Tillinghast JS, Sinku A, Liu C, ain B, Dickson M, Mize NK, Nishikawa M;

WPI; 2001-657166/75.

N-PSDB; AAD21740

Stache-Crain B,

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(HYSE-) HYSEQ INC. (KIRI) KIRIN BEER

05-APR-2000; 2000US-00543774. 28-JUN-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757562. 05-FBB-2001; 2001US-0266614P.

05-APR-2001; 2001WO-US011208

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The nucleotide sequence (NS) of the full-length protein-coding sequence of clones ci254 (AAV831312, da2286 (AAV83133), du4105 (AAV83134), eh801 (AAV83135), er3691 (AAV83136), fh1235 (AAV83137), fm601 (AAV83138) or fr4732 (AAV83139), (all clones are deposited as ATCC 98415) and the proteins they encode are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals for example, tumour suppression/invasion activity, immune system boosting activity. The polynucleotides are also believed to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; viruotide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; ejammaglobulnaemia; thalassaemia; dauplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immune deficiency syndrome; agammaglobulnaemia; thalassaemia; daucher; disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaemia; SCID; severe combined immunodeficiency; immune disorder; antoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LGKCLDNCPEGLEANNHTFGCVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREIIQ 181
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                                         New polynucleotides encoding secreted human proteins - are derived from human foetal brain, adult brain, adult blood or placenta CDNA libraries, useful, e.g. as potential immunomodulators.
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                                                                                                                                  Claim 8; Page 63-64; 104pp; English.
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, or germ cell, germ line stem cell, embryonic stem cell, paramile stem cell, embryonic stem cell, paramile stem cell embryonic stem cell, paramile stem cell proposition cell, paramile stem cell proposition cell, paramile stem cell provents cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell cator-like proteins can replace as a graft for the bone marrow crowth seases such as immunodeficiency syndrome, chronic granulomatous diseases utplicated immunodeficiency syndrome, chronic granulomatous wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AlDS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia cuch as sickle cell anaemia due to enzyme defect, congenital anaemia desentation, a variety of cancer and tumours. Proteins of the invention cell sease and other neurodegenerative diseases, thrombocytopeania, immune deficiencies and disorders such as severe combined immune deficiency syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is human SCR-1 related protein
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                                                                                                                                                                                                                                                                                                                                                                                  Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Page 231-232; 232pp; English.
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Matches 264; Conservative
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Treacy M,
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                                                                                   TREACY M.
SPAULDING V.
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                                                                              EVANS C.
MERBERG D.
                                                                    JACOBS K.
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                                                               18-MAR-1998;
                                             Homo sapiens.
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                                                                                          Jacobs K,
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WPI; 2003-381616/36 WO2003029405-A2. Homo Bapiens .0-APR-2003. ABR62114; 63 183 Query Match rang YT; RESULT 19 8888888888888888 ð 셤 8 셤 셤 ð 셤 ò ò The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary decyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or preventing a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antinflammatory, stem cell growth factor activity and activin or inhibin-related cryokine. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, autoimmune diseases and neuropathies, such as that the properties of the treatment of central and peripheral nervous system diseases and neuropathies, such as that a clare or by Parkinson's disease, fluttington's disease, amyotrophic attains a clerosis. (I) is involved in chemotactic or chemokinetic activity, regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaemia Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulocer; fungicide; antidabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy. Novel secreted or transmembrane protein and polymucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis. Evans C; Collins-Racie LA, Claim 207; Page 203-204; 284pp; English KEIPEQRENKQQQKKRKVQDKQKS 265 Lavallie ER, C ABP61846 standard; protein; 292 Human polypeptide SEQ ID NO 200 22-DEC-2000; 2000US-00745763. 98US-00040963 MCCOY J M. LAVALLIE E R. COLLINS-RACIE L A. 04-OCT-2002 (first entry) 셤

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and for regeneration of bone, cartilage, tendon, ligament and/or nervetissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoprosis, osteoarthritis, bone degenerative disorders or periodontal disease. (1) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.1%; Score 1472; DB 5; I. 100.0%; Pred. No. 1.2e-107; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 KEIPEQRENKQQQKKRKVQDKQKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR62114 standard; protein; 292 AA
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10-DBC-2001; 2001US-0339739P.
19-APR-2002; 2002US-00125852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 292 AA;
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The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerating different cell types, for treating e.g. leukaemia, haemophilia and degenerating mew tissues and organs that consistent of patients in need of transplanted tissues. The polynucleotides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in consistent of generating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically chind the polypeptide as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current cor prevention of cancers, and other immunological disorders. The current cor prevention of cancers, and other immunological disorders. The current cor prevention of ancers, and other immunological disorders.
                      New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
                                                                                                                                                  Disclosure; Fig 2; 151pp; English
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PPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 122 LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182 62 PPALERIGMEQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNRNFCFKCKSGFYLH 121 61 3 HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCXPRL 62 Gaps ő 97.1%; Score 1472; DB 6; Length 292; 100.0%; Pred. No. 1.2e-107; tive 0; Mismatches 0; Indels (Best Local Similarity 100. Matches 264; Conservative 123 63 122 Query Match ઠ 엽 Š 셤 õ 요 ð 셤 ò

Search completed: June 29, 2004, 16:59:51 Job time : 66.6986 secs

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ALIGNMENTS

Sequence Seq

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19 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFFALERIGMKQIGV
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08284941

APPLICANT: BARR, PHILIP J
APPLICANT: RIBER, PHILIP J
APPLICANT: RIBER, PHILIP J
APPLICANT: BARR, PHILIP J
APPLICANT: BARR, PHILIP J
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS NUMBERS OF SEQUENCES.
ICTILE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS CORRESPONDENCE ADDRESSES.
CORRESPONDENCE ADDRESS:
ICTILE PALO ALTO SQUARE
CONDUTRY: USA
STATE: CALIFORNIA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBMP C compatible
OPERATION SYSTEM: US/08/284,941
FILING DATE: 2 AUGUST 1994
CLASSIFICATION NUMBER: US/08/284,941
FILING DATE: 3 AUGUST 1994
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION POR SEQ ID NO: 2:
SEGUENCE CHARACTERIFICE:
SEGUENCE CHARACTERIFICE:
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11.4%; Score 173.5; DB 2; Length 969;
Best Local Similarity 28.8%; Pred. No. 1.2e-06;
Matches 44; Conservative 16; Mismatches 54; Indels 39
LENGTH: 969 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Sequence 2, A
Sequence 23,
Sequence 21,
Sequence 21,
Sequence 21,
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1516
1 MGHLRLISWLFIILNFWEYI......QQXKRKVQDKQKSVSVSTVH 273
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgm2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-525-940-18
US-08-976-838-18
US-08-976-838-18
US-09-214-555B-7
US-09-214-555B-7
US-09-207-754A-4
US-09-907-754A-4
US-09-907-75A-4
US-08-95-940-15
US-08-525-940-15
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US-08-976-838-15
US-09-205-258-441
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US-08-185-432-18
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PCT-US93-03164-12
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                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Gaps

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US-09-236-503-2
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                                             19 YIGSONASRGRRORRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFPALERIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08447642

Sequence 2, Application US/08447642

Partent No. 5989890

GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: KIRFER, MICHARL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND FOLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.4%; Score 173.5; DB 2; Length 969; Best Local Similarity 28.8%; Pred. No. 1.2e-06; Matches 44; Conservative 16; Mismatches 54; Indels 39
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ANNHIMBCVSIVHCEVSEWNPWSPCTKKGKTCG 168
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APPLICATION DATA

APPLICATION NUMBER: US 08/284,941

FILING DATE: 2 August 1994

FILING DATE: 2 August 1994

ATTORNEY/AGENT INFORMATION:

NAME: NEBLEY PH.D., RICHARD L.

REGISTRATION NUMBER: 30092

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 843-5070

TELEPHONE: (415) 863-5070

TELEPHONE: (415) 863-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                              US-08-447-642-2
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RESULT 3 US-09-236-503-2

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GENERAL INFORMATION:
APPLICANT: Barr, Philip J
APPLICANT: Richer, Michael C
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Polypeptides in Cells
FILE REFERENCE: CHIR-O09/0408
CURRENT APPLICATION NUMBER: US/09/236,503
CURRENT PILING DATE: 1999-01-25
EARLIER APPLICATION NUMBER: 08/447,642
EARLIER PILING DATE: 1995-05-23
EARLIER PILING DATE: 1994-08-02
EARLIER PILING DATE: 1992-03-09
WUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 YIGSQNASRGRRQRRWHPNVSQGCQGCATCSD--YNGCLSCKPRLFFALBRIGMKQIGV 76
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; Sequence 2, Application PC/TUS9302147A
; GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: RIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND TITLE OF INVENTION: DECK 4.1 GENE AND POLYPEPTIDES IN CELLS NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: PIVE PALO ALTO SQUARE
CITY: PALO ALTO
CITY: PALO ALTO
STREET: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 173.5; DB 3; Length 969; 28.8%; Pred. No. 1.2e-06;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 ANNHIMECVSIVHCEVSENNPWSPCTKKGKTCG 168
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REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
Sequence 2, Application US/09236503
Patent No. 6277590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 2
LENGTH: 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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us-09-894-912a-13.rai

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PILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            164 GKTC-----GFKRGTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 799 amino acids
amino acid
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Matches 55, Conservative
                       ; MOLECULE TYPE: protein US-08-525-940-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                 Query Match
Best Local Similarity
Matches 55; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 QRKKCQK 209
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      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-976-838-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                   19 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLFFALERIGMKQIGV 76
                                                                                                                                                                                                                                             11.4%; Score 173.5; DB 5; Length 969; 28.9%; Pred. No. 1.2e-06; tive 16; Mismatches 54; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Frankusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                     54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/368,852
FILING DATE: 01-7AN-1995
PRIOR APPLICATION UNDER: US 08/088,322
APPLICATION UNDER: US 08/088,322
FILING DATE: 07-UL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE! DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2848-11-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/08525940 Patent No. 5866351 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 799 amino acide TYPE: amino acide
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-063
TELEX: 380816 COOLEY PA
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
                                                                                                                         LENGTH: 969 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 FDSELIRCGECHH----
                                                                                                                                                                                                                                                                  Best Local Similarity 28.8
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                       PCT-US93-02147A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-525-940-23
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                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                               138 NHTME-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                 ----TRVREIIQHPSAKGNLCPPTNETRKCTV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          725 DISCLICNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATERSWAEGGFCMLVKKKNNLC-- 782
                                                                                                                                                                                                                                                       609 THCPDGSYQDTKK---NLCRKCSENCKTCTEPHNCTECRDGLSLQGSRCSVSCEDGRYFN
                                                                                                          21 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFPALERIGMKQIGVCL
                                                                                                                                                               563 GHYHADK-KRCRKCAPN-----CESCFGSHGDQCMSCKYGYFL----NEETNSCV
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                          78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
GENERAL INFORMATION:
TPILE OF INVENTION: CD4 F-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 162; DB 2; Length 799; 22.3%; Pred. No. 9.4e-06; tive 33; Mismatches 81; Indels 7
ch 10.7%; Score 162; DB 2; Length 799; 1 Similarity 22.3%; Pred. No. 9.4e-06; 55; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Derver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEADEL PC-DOS/NS-DOS
SOFTARE: PATENT: PC-DOS/NS-DOS
SOFTARE: PATENT: Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/976,838
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645 GHYHADK-KRCRKCADN-----CBSCFGSHGDQCMSCKYGYFL-----NBETNSCV 689
                                                                                                                  138 NHTMB-----NPWSPCTKK 163
                                                                                                                                                                                                                      747 GODCOPCHRPCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYPDHSSENGYKSCKKC 806
                                                                                                                                                                                                                                                                     164 GKTC-----GFKRGTB------TRVRBIIQHPSAKGNLCPPTNETRKCTV 202
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                                                                                                                                                                                                                                                                                                               807 DISCLICNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATEBSWAEGGFCMLVKKNNLC-- 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLALGKCLDNCPEGLEAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLPPALBRIGMKQIGVCL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMXQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Francusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
OVERSES OF SEQUENCES: 31
CORRESPONDENCES: 32
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.7%; Score 162; DB 2; Length 881; Best Local Similarity 22.3%; Pred. No. 1e-05; Matches 55; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION WHBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHAN: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS LENGTH: 881 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-976-838-21
                                                                                                                                                                                                                                                                                                                                                           203 QRKKCQK 209
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                                                                                                                    138 NHTME-----NPWSPCTKK 163
                                                                                                                                                                                                             -----TRVREIIQHPSAKGNLCPPINETRKCTV 202
                                                                                                                                                                                                                                                                                                   19 SSCPSG-YYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 137
  21 GSQNASRGRRORRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08525940
Fatent No. 5866551
GENERAL INFORMATION:
FAPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Molf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.7%; Score 162; DB 2; Length 881; Best Local Similarity 22.3%; Pred. No. 1e-05; Matches 55; Conservative 33; Mismatches 81; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILLING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 2848-11-C1
RELEPHONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFAX: (303) 863-9700
                                                                                                                                                                                                                                                                       164 GKTC-----GFKRGTB-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 881 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-940-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                              203 QRKKCOK 209
                                                                                                                                                                                                                                                                                                                                                                                                          783 ÖRKVLÖQ 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-08-525-940-21
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781 GODCOPCHRFCATCAGAGADGCINCTEGYPMEDGRCVOSCSISYYPDHSSENGYKSCKKC 840
                                                                                   ---TRVREIIQHPSAKGNLCPPTNETRKCTV 202
                                                                                                           79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 NHTME-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 DISCLITCNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATBESWARGGFCMLVKKNNLC-- 898
  ---IVHCEVSEW-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 GKTC-----GPKRGTE-----TRVREIIQHPSAKGNLCPPTNETRKCTV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      679 GHYHADK-KRCRKCAPN-----CESCFGSHGDQCMSCKYGYFL-----NEFTNSCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GSQNASRGRRQRRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFPALERIGMKQIGVCL
                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPANDED TITLE OF INVENTION:
CORRESPONDENCE 31
CORRESPONDENCE 31
CORRESPONDENCE Sharidan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 162; DB 2; Length 915; 22.3%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REPREMENCE FOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPRA: (303) 863-9700
ITELEPRA: (303) 863-923
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                 164 GKTC-----GFKRGTB
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amino acid
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Matches 55; Conserva
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  138 NHTMB--
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                                                                                                                                                                                                                                                                       RESULT 10
US-08-976-838-18
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----IVHCEVSEW-----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GSONASRGRRORRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGWKQIGVCL 78
                                                                                                           : : : | | | : : : B07 DISCLTCNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATEESWARGGPCMLVKKNNLC--
                                                                                   ---TRVREIIQHPSAKGNLCPPTNETRKCTV
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT.
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/525,940
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1700 Lincoln Street, Suite 3500
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-0AN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-UL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
138 NHTME-----CVS-
                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08525940 Patent No. 5866351 GENERAL INFORMATION:
                                                                              164 GKTC-----GFKRGTB
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les 55; Conservative
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STREET: L. TTTY: Denver
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/ MOLECULE TYPE: protein
US-08-368-852-15
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STATE: CO
COUNTRY: U.S.A.
**TO: 80203
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 162; DB 4; Length 915;
; Pred. No. 1.1e-05;
33; Mismatches 81; Indels
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Patent No. 6380171
GENERAL INPORMATION:
PAPLICAMT: INPORMATION:
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT FILING DATE: 1999-01-04
PRIOR FILING DATE: 1999-01-04
PRIOR FILING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-25
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                      APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILE REFERENCE: PRO-PROTEIN CONVER ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT APPLICATION NUMBER: 06/021,008
FRIOR APPLICATION NUMBER: 60/021,008
PRIOR FILING DATE: 1997-07-26
PRIOR FILING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGH: 915
                                                                                                          Sequence 2, Application US/09214555B Patent No. 6380171 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%;
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Best Local Similarity 22.3%
Then 55; Conservative
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; ORGANISM: Homo sapiens
US-09-214-5558-7
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; ORGANISM: Homo sapiens
US-09-214-5558-2
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QRKKCQK 209
                                899 QRKVLQQ 905
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US-09-214-555B-2
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US-09-214-555B-7
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                                                                                                                                 79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 137
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                                                78; Gaps
                                                                                                21 GSQNASRGRRQRRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALBRIGMKQIGVCL
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Query Match 10.7%; Score 162; DB 4; Length 915; Best Local Similarity 22.3%; Pred. No. 1.1e-05; Matches 55; Conservative 33; Mismatches 81; Indels
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Patent No. 569183
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Practausoff, Alex
APPLICANT: Miranda, Luis R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
NUMBER OF EQUENCES: 15
CORRESPONDENCE: 15
CORRESPONDENCE: 15
CORRESPONDENCE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,852
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435
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10.6%; Score 161; DB 1;
Best Local Similarity 28.2%; Pred. No. 3.6e-06;
Matches 46; Conservative 25; Mismatches 52.
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REGISTRATION NUMBER: 37,459
REPERENCE/DOCKET NUMBER: 2848-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SRQ ID NO: 15: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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APPLICANT
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                                                                           94 NKCTKCKADCDTCPNK--NPCTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSIVHC 149
PRCSEVGCDGPGPDHCND---CL---HYYYKLK----NWTRICVSSCPPGHY---HADK 58
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/20594
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Grimaldi, Christopher J.
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary B.
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                                                 10.5%; Score 158.5; DB 4; Length 379; 24.9%; Pred. No. 8.1e-06; Live 26; Mismatches 72; Indels 83
| PRIOR PILING DATE: 1999-12-16
| PRIOR APPLICATION NUMBER: PCT/US99/30911
| PRIOR PILING DATE: 1999-12-20
| PRIOR PILING DATE: 1999-12-20
| PRIOR PILING DATE: 1999-12-20
| PRIOR APPLICATION NUMBER: PCT/US99/3099
| PRIOR PILING DATE: 2000-01-05
| PRIOR PILING DATE: 2000-01-05
| SEQ ID NO 4
| LENGTH: 379
| TYPE: PRT
| CRGANISM: HOMO Bapien8
| US-09-907-794A-4
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CURRENT APPLICATION NUMBER: US/09/905,125A
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
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Gao, Wei-Qiang
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Baton, Dan L.
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Best Local Similarity
Matches 60; Conserva
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Query Match 10.5%; Score 158.5; DB 4; Length 379;
Best Local Similarity 24.9%; Pred. No. 8.1e-06;
Matches 60; Conservative 26; Mismatches 72; Indels 83; Gaps 16;
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR FLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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Job time : 16.2464 secs
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Sequence 24, Appl
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Sequence 166, Appl
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2: /cgn2_6/ptodata/1/pubpaa/PCT_REW PUB.Popp:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_REW PUB.Popp:*

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Maximum Match 100%
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US-10-087-192-1779 Sequence 1779, Ap US-09-984-912A-14 Sequence 17, Appl US-10-276-774-1744 Sequence 11, Appl US-10-125-952-18 Sequence 21, Appl US-10-125-952-21 Sequence 22, Appl US-10-125-952-34 Sequence 25, Appl US-10-185-770-2 Sequence 25, Appl US-10-185-852-13 Sequence 12, Appl US-10-125-852-3 Sequence 12, Appl US-10-125-852-3 Sequence 12, Appl US-10-125-852-13 Sequence 12, Appl US-10-125-852-9 Sequence 13, Appl US-10-125-852-9 Sequence 14, Appl US-10-125-852-9 Sequence 17, Appl US-10-125-852-9 Sequence 20, Appl US-10-125-852-9 Sequence 20, Appl US-10-125-852-1 Sequence 21, Appl US-10-125-852-1 Sequence 21, Appl US-10-125-852-1 Sequence 21, Appl US-10-125-852-1 Sequence 21, Appl US-10-135-852-1 Sequence 21, Appl US-10-135-852-1 Sequence 2, Appl US-10-357-820-8 Sequence 6, Appl US-10-357-820-8 Sequence 6, Appl US-10-357-820-8 Sequence 6, Appl US-10-357-820-1 Sequence 6, Appl US-10-357-820-1 Sequence 6, Appl US-10-357-820-1 Sequence 10, Appl US-10-357-820-1 Sequence 6, Appl US-10-357-820-1 Sequence 10, Appl US-10-357-820-1 Sequence 6, Appl US-10-357-820-1 Sequence 10, Appl US-10-357-820-1 Sequence 6, Appl US-10-357-820-1 Sequence 10,	ELATING TO NOVEL STE	.6; DB 10; Length 273;
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981 903 903 903 656 628 638 638 638 574 577 577 577 577 577 577 577 577 577	SEULT 1 Sequence 13, Application US/0989 Publication No. US20030044792A1 GERERAL INFORMATION: APPLICANT: Tang et al. TITLE OF INVENTION: METHODE AND FRICK PLING DATE: 2001-02-05-18 PRIOR PILING DATE: 2001-02-05 PRIOR APPLICATION NUMBER: 60/21 PRIOR APPLICATION NUMBER: 60/21 PRIOR PILING DATE: 2000-06-28 PRIOR PILING DATE: 2000-06-38 PRIOR PILING DATE: 2000-06-38 PRIOR PILING DATE: 2000-06-38 TUMPER OF SEQ ID NOS: 48 SOFTWARE: PAT INGO 33 TYPE: PRT TYPE: PRT ORGANISM: Home sapiens	Match
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APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 28110/37260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT FILING DATE: 2001-06-05

FRIOR PLING DATE: 2001-04-05

FRIOR PLING DATE: 2001-04-05

FRIOR PLING DATE: 2000-06-28

FRIOR PLING DATE: 2000-06-28

FRIOR PLING DATE: 2000-06-28

FRIOR PLING DATE: 2001-01-09

FRIOR PLING DATE: 2001-01-09
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: Sequence 10, Application US/09894912A
: Publication No. US20030044792Al
; GENERAL INFORMATION:
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US-09-894-912A-34 ; Sequence 34, Application US/09894912A

RESULT 3

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US-10-125-852-23

US-10-125-852-23

Sequence 23, Application US/10125852

Sequence 23, Application No. US20030032034A1

SEQUENCE STATE SEQUENCE OF SEQUENCE OF SEQUENCE STEM CELL GROWTH FACTOR-1

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION NUMBER: US 60/316,368

PRIOR FILING DATE: 2001-08-30

PRIOR FILING DATE: 2001-08-30

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.1

LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                            GERREAL INFUGENTION:
GERREAL INFUGENTION:
GERREAL INFUGENTION:
FILLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL;
TITLE OF INVENTION: PRACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 28110/372504
CURRENT APPLICATION NUMBER: US/09/894,912A
CURRENT APPLICATION NUMBER: US/09/894,912A
CURRENT FILLING DATE: 2001-04-05
PRIOR PELING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/266,614
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-05
PRIOR PELING DATE: 2000-04-05
PRIOR PELING DATE: 2000-04-05
PRIOR SEQ ID NOS: 48
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 34
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 1505; DB 10; Length 272; 100.0%; Pred. No. 1.3e-114; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 KEIPEQRENKQQQXKRXVQDKQXSVSVSTVH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 KEIPEQRENKQQXKRKVQDKQKSVSVSTVH 272
Publication No. US20030044792A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-852-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-894-912A-34
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HPSAKGNLCPPTNETRKCTVQRKKCQXGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 242
182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg, David
Treacy, Maurice
Spaulding, Vikh
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.1%; Score 1472; DB 9; I Best Local Similarity 100.0%; Pred. No. 6.6e-112; Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-745-763-166
                                                    243 KBIPBORENKOOOKKRKVODKOKS 266
                                                                                                    242 KEIPBORENKOOOKKRKVODKOKS 265
                                                                                                                                                                                                                                                                                                                                McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           Sequence 166, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                         US-09-745-763-166
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APPLICATT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 28110/37250A

CURRENT PILING DATE: 2002-05-10

PRIOR PELING DATE: 2001-04-05

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-01-09

PRIOR PELING DATE: 2001-01-09

PRIOR PELING DATE: 2001-01-09

PRIOR PELING DATE: 2000-04-05

WINDER OF SEQ ID NOS: 48

SOFTWARE: PACENTIN NUMBER: 09/543,774

PRIOR FILING DATE: 2000-04-05

HENDR PILING DATE: 2000-04-05

BRIOR PILING DATE: 2000-04-05

HENDR PILING DATE: 2000-04-05
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                                                                                                                                                              2 HLRLISWLFIILINFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPRL
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                                                                                                                            3 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
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                             Score 1505; DB 14; Length 272; Pred. No. 1.3e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 265;
                                                                          Indels
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100.0%; Pred. No. 5.9e-112;
iive 0; Mismatches 0;
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                                            100.0%; Pred. ...
rive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-894-912A-26
, Sequence 26, Application US/09894912A
, Publication No. US20030044792A1
, GENERAL INFORMATION:
                          99.38;
                     99.3%
Query Match
Best Local Similarity 100.0
Matches 271; Conservative
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Best Local Similarity 100.
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Homo sapiens US-09-894-912A-26
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US-09-94-912A-16

Sequence 16, Application US/09894912A

Sequence 16, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICATION NO. US20030044792A1

GENERAL INFORMATION:

TITLE OF INVERTION:

TITLE OF INVERTION WHORER: US/09/094,912A

CURRENT FILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2000-04-05

NUMBER: 09/543,774

PRIOR PILING DATE: 2000-04-05

NUMBER: 09/543,774

PRIOR PILING DATE: 2000-04-05

SEQ ID NO 16

SEQ ID NO 16

LEWSTH: 251

LEWSTH: 251

LEWSTH: 251

TYPER: DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PFALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGPYLH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
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                                                                                                                                                                                                                                                                                                                                            Length 292;
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97.1%; Score 1472; DB 14;
Best Local Similarity 100.0%; Pred. No. 6.6e-112;
Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.1%; Score 1400; DB 10; Best Local Similarity 100.0%; Pred. No. 4.1e-106; Matches 251; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2001-08-30
PRIOR PELICALION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 KBIPEQRENKQQQKKRKVQDKQKS 266
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ORGANISM: Homo sapiens
US-09-894-912A-16
                                                                                                                                                                                                                     TYPE: PRT
GRGANISM: Homo sapiens
US-10-125-852-25
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Publication No. US20030032034A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH PACTOR-I
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-43A
CURRENT APPLICATION NUMBER: US/10/125,852
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/316,368
                                                                                                                                                                                                               RESULT 7

US-09-894-912A-48

Sequence 48, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICANT Tang et al.

TITLE OF INVENTION:

FILLE REPERENCE: 28110/37260A

CURRENT PAPLICATION NUMBER: US/09/894,912A

CURRENT PILING DATE: 2002-05-10

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-01-02

PRIOR PILING DATE: 2001-01-02

PRIOR PILING DATE: 2001-01-03

PRIOR PILING DATE: 2001-01-03
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         182 HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESS 241
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                                                                        243 KEIPEORENKOOOKKRKVODKOKS 266
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US-10-125-852-25
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Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICANT: Tang et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

FALTOR OF INVENTION:

CURRENT APPLICATION WINBER: US/09/894,912A

CURRENT APPLICATION NUMBER: To be assigned

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR APPLICATION NUMBER: 60/266,614

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2001-04-05

PRIOR PILLING DATE: 2000-06-28

PRIOR PILLING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 32

LEAGTH: 279
183 HPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKE--AIPDSKS 238
                                                                                          202
                                                                                                               181 QRXKCQKGERGKKGRERKRKKKPNKGESKEAIPDSKSLESSKEIPBQRENKQQQKRRVQD 240
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                                                                                       143 CVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTV
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US-09-894-912A-32
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US-09-894-912A-32
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RESULT 11 US-10-185-770-4

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Sequence 4, Application US/10185770
Publication No. US20030022217A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
GURRENT APPLICATION NUMBER: US/10/185,770
CURRENT APPLICATION NUMBER: 60/301,852
PRIOR PILING DATE: 2001-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
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; Bequence 1782, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
    TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER.
    FILE SPERENCE: 229452000122
    CURRENT APPLICATION NUMBER: US/10/087,192
    CURRENT FILING DATE: 2002-03-01
    PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR PILLING DATE: 2000-12-22
    PRIOR PILLING DATE: 2001-03-02
; RIUNG PALLICATION NUMBER: US 09/798,586
    PRIOR PILLING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FaetSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1275; DB 14; Pred. No. 5.5e-96;
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100.0%; Pred. No. 5...
'... 0; Mismatches
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 4
SOCITIVARES: PastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 225
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US-10-087-192-1782
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-087-192-1782
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APPLICANT: Zhong, Mei
IITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
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                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                              2 HIRLISWIPTIINFWEYIGSQNASRGRRQRRWHPNYSQGCQGGCATCSDYNGCLSCRPRL 61
                                                                                                                                                                                                                                                                    3 HIRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                        4
                                                                                                                                                                             Length 239;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                           Score 1178; DB 15;
Pred. No. 4.6e-88;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 BIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGBRG 213
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CURRENT APPLICATION NUMBERS: US/10/094,886
CURRENT FILING DATE: 2002-03-07
PRIOR PELING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR APLICATION NUMBER: 60/313,182
PRIOR APPLICATION NUMBER: 60/288,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 176, Application US/10094886 Publication No. US20040002120A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Buturajan, Meera
APPLICANT: Breess, Catherine
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Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li, Li
Gorman, Linda
Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
                                                                                                                                                                                77.78;
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Gangolli, Esha
Gusev, Vladimir
Smithson, Glamda
Zerhusen, Bryan
Gerlach, Valerie
                                                                                                                                                                             Query Match
Best Local Similarity 97.7
Matches 210; Conservative
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NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 172
LENGTH: 239
                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-886-172
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US-10-094-886-176
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAMB, AND METHOD
FILE REPERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
CURRENT PILING DATE: 2002-03-07
PRIOR PLILNG DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-06-07
PRIOR PRIOR PLING DATE: 2001-06-07
  139 LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFRRGTETRVREIIQ 198
                                                                                           LGKCLDNCPEGLEANNHTFMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
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Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRK 222
                                                                                                                                                                                                         HPSAKGNLCPPTNETRKCTVQRKKCQKGERGTIIGEEKKK 239
                                                                                                                                                                                                                                                                                                                                 Sequence 172, Application US/10094886
Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Rekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Vernet, Corine A.
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Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
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Spaderna, Steven
LaRochelle, William
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Gangolli, Esha
Gusev, Vladimir
Smithson, Glemnda
Zerhusen, Bryan
Gerlach, Valerie
Pochart, Vascal
Pernandes, Elma
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Malyankar, Uriel M.
Boldog, Perenc
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US-10-094-886-172
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                  PRIOR APPLICATION NUMBER: 60/318,510
PRIOR FILING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-01
PRIOR PLING DATE: 2001-03-08
PRIOR PLILATION NUMBER: 60/274,281
PRIOR PLILATION NUMBER: 60/314,018
PRIOR PLILOG DATE: 2001-08-21
PRIOR PLILOG DATE: 2001-03-08
PRIOR PLILOG DATE: 2001-03-09
PRIOR PLILOG DATE: 2001-08-21
PRIOR PLILOG DATE: 2001-08-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: 0F SEQ ID NOS: 298
SOFTWARE: PALENTIN 2.1
SEQ ID NO 176
LERNOTH: 195
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Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Vernet, Corine A.
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Boldog, Perenc
Guo, Xiaojia
Shenoy, Suresh
Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
FILING DATE: 2001-05-02
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Zerhusen, Bryan
Gerlach, Valerie
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Gangolli, Esha
Gusev, Vladimir
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Gorman, Linda
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ORGANISM: Homo sapiens
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APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Spaderna, Steven
APPLICANT: LaRochelle, William
APPLICANT: LaRochelle, William
APPLICANT: LaRochelle, William
APPLICANT: Larochelle, William
FILE OF INVENTION: THERAPERTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
FILE OF INVENTION: THERAPERTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
FILE REPERENCE: 21402-290 B
CURRENT FILING DATE: 2001-03-03
FRIOR PLING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: 60/218,182
FRIOR PLING DATE: 2001-05-02
FRIOR PLING DATE: 2001-05-02
FRIOR PLING DATE: 2001-03-08
FRIOR PLING DATE: 2001-03-08
FRIOR PLING DATE: 2001-08-21
FRIOR PLING DATE: 2001-06-07
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR PLING DATE: 2001-06-07
FRIOR APPLICATION NUMBER: 60/214,194
FRIOR PLING DATE: 2001-06-07
FRIOR PLING DATE: 2001-06-07
FRIOR PLING DATE: 2001-06-07
FRIOR PLING DATE: 2001-06-07
FRIOR FILING PLICATION MUMBER: 60/313,626
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Job time: 40.7755 secs
Fernandes, Blma
Shimkets, Richard
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Best Local Similarity 99.55
Matches 192; Conservative
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US-10-094-886-174
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June 29, 2004, 16:56:05; Search time 13.915 Seconds (without alignments) 1887.186 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

US-09-894-912A-13 1516 1 MGHLRLISWLFIILNFWEYI......QQKKRKVQDKQKSVSSTVH 273 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	furin (BC 3.4.21.7	serine proteinase	subtilisin-like pr	subtilisin-like pr	furin (BC 3.4.21.7	subtilisin-like pr	probable proprotei	PACE4A - mouse (fr	subtilisin-like pr	subtilisin-like pr	subtilisin-like pr	hypothetical prote	Whit inhibitory fac	gene PACE4 protein	F-spondin precurso	protein bli-4D [im	Motch B protein -		Xotch protein - Af	cell-fate determin	probable kexin (BC	hypothetical prote	F-spondin - rat	Wnt inhibitory fac	trophozoite cystei	insulin-like growt	notch protein homo	protein-tyrosine k	notch protein homo
SUMMARIES	ID	T43251	S34583	JC5571	JC5570	A43434	A39490	B48225	152527	A48225	G02428	JC6148	T24232	A59180	153282	A47723	D87803	A49175	A33837	A35844	A49128	T37314	T27283	A38152	B59180	C42125	IGHUR1	A40043	870713	S18188
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مد	Query	12.7	12.3	12.1	12.1	11.6	11.4	11.1	11.0	11.0	10.7	10.7	10.6	10.5	10.3	10.3	10.1	9.9	9.8	9.6	9.7	9.6	9.6	9.5	9.4	9.4	9.5	9.5	9.1	9.1
	Score	192	186.5	184	184	176.5	173.5	LO.	167.5	167	162	162	161	158.5	156.5	156	153.5	150.5	149	148.5	147.5	145	145	143.5	142	142	139	139		138
•	Regult No.	٦	7	٣	4	2	9	7	8	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

notch-1 protein -	transmembrane prot	insulin receptor-r	insulin receptor p	hypothetical prote	insulin receptor p	insulin receptor p	insulin receptor (insulin receptor -	apoptosis-mediatin	insulin receptor-r	Notch homolog Motc	hypothetical prote	trophozoite surfac	furin (BC 3.4.21.7	cysteine rich prot
19	12	17	PK.	972	157	080	245	181	184	502	325	112	179	256	42017
A46019	S426	B47417	DHN:	T26	\$	A36	857	A56081	A46	B36	A486	T22812	A485	843656	T42
2 A460	2 \$426	2 B474	1 INHO	2 T26	2 A34	2 A36	2 857	1 A56(2 A46	2 B369	2 A486	2 T228	2 A485	2 5436	2 T42
~	ď	N	-	N	N	N	~	H	N	N	N	3871 2 T228	N	0	2
~	ď	540 2	1382 1	1111 2	1372 2	1383 2	21012	2148 1	327 2	N	861 2	3871 2	N	0	2
9.1 2531 2	ď	9.0 540 2	8.9 1382 1	8.9 1111 2	8.9 1372 2	8.9 1383 2	8.5 2101 2	2148 1	8.4 327 2	8.4 1268 2	861 2	8.3 3871 2	8.3 667 2	0	8.2 1274 2 1

ALIGNMENTS

Gerine proteinase (BC 3.4.21.-) PC6B - mouse cispecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacte: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S34583
R;Nakagawa, T.; Murakami, K.; Nakayama, K.
FRBS Lett. 377, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a } A;Reference number: S34583; MUID:93327934; PMID:8335106

RESULT 2 S34583

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C;Accession: JC5570

F; Ni, S; Kii, S; Tsuji, A; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Ni, B;Acchem. 121, 941-948, 1997

A;Title: A novel human PACB4 isoform, PACB4B is an active processing protease containing A;Title: A novel human PACB4 isoform, PACB4B; PMID:9192737

A;Reference number: JC5570; MUID:97335942; PMID:9192737

A;Accession: JC5570

A;Status: nucleic acid sequence not shown
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B,Experimental source: brain cerebellum
C;Comment: This enzyme is a processing protease and responsible for processing of varion of it is retained intracellularly.
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R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, B.
B;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, B.
Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc A;Reference number: A43434; MUID:92381036; PMID:1512259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subrilisin-like proprotein convertase (BC 3.4.21.-) PACB4 precursor, splice form B-I C;Species: Homo sapiens (man) C;Species: 23-Sep-1997 #sequence_revision 24-Sep-1997 #sequence_revisio
                                                                                                                                                                                                                           825 FDSELIRGGECHHTCGTCVGPGREECIHCAKNPHFHDW----KCVPACGEGFYPE---- 875
                                                                                                                   136 ANNHIMEC------VSIVHCEVS-EWNPWSPCTKKGKTCGFKRGTETRVRE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             737 YFGDTAARRCRR-----CHKGCETCSSRAATQCLSCR-RGFY-----HHQEMNT 779
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767 CVTLCPAGFYADE--SQKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY 824
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C; Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C; Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C; Superdamily: subtilisin-like protein predicted sIG>
P; 1-62/Domain: signal sequence #status predicted cAIG>
P; 63-149/Domain: propeptide #status predicted cPRO>
P; 196-434/Domain: propeptide #status predicted cPRO>
P; 196-434/Domain: propeptide momology cABT>
P; 196-434/Domain: propeptide momology cABT>
P; 196-434/Domain: protein site: App, His, Asn, Ser #status predicted
P; 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C,Species: Drosophila melanogaster
C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 PDSRLIRCGECHHTCGTCVGPGREECIHCAKNFHFHDW----KCVPACGEGFYPB----
                                                                                                                                                                                                                                                                                                                                                                                                                             876 --EMPGLPHKVCRRYGPPGGB-RQATVS----SKGVPG--GQSLSASSPGAGE 919
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A,Cross-references: GDB:131390; OMIM:167405
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A; Residues: 1-975 < MOR>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Sacession: JG5571
R; Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na J. Biochem. 121, 941-948, 1997
J. Biochem. 121, 941-948, 1997
A; Fitle: A novel human PACE4 isoform, PACE4E is an active processing protease containing A; Reference number: JG5570; MUID:97335942; PMID:9192737
A; Accession: JG5571
A; Status: nucleic acid sequence not shown
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                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-1548 <NAK>
A,Cross-references: GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C,Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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A,Residues: 1-962 **MOXA-
A);Cross-references: DDBJ:D87994; NID:g2330550; PIDN:BAA21792.1; PID:g2330551
A,Experimental source: brain cerebellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 SQCCQGCCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDI--N
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A;Rmap position: 15q26-15q26
C;Superfamily: subtiliain-like proteinase PACB4; subtilisin homology
C;Superfamily: subtiliain-like proteinase
F;1-62/Domain: signal sequence #status predicted <SIG>F;1-62/Domain: propeptide #status predicted <PRO>F;196-434/Domain: propeptide #status predicted <PRO>F;393-954/Domain: hydrophobic cluster #status predicted <HCL>F;383-954/Domain: hydrophobic cluster #status predicted <PCO>F;393-954/Domain: hydrophobic cluster #status predicted <PCO>F;393-954/Domain: hydrophobic cluster #status predicted <PCO>F;398-954/Domain: hydrophobic cluster #status predicted <PCO>F;398-954/Domain: hydrophobic cluster #status predicted <PCO>F;398-954/Domain: hydrophobic cluster #status predicted 
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                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 186.5; DB 2; Length 1
25.0%; Pred. No. 6.8e-05;
-ive 31: Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Conservative
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Best Local Similarity
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Best Local Similarity
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                  Accession:
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C;Accession: B48225
R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop
A;Reference number: A48225; MUID:93342056; PMID:8341687
A;Recession: B48225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:L14933
C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Superfamily: subtilisin-like proteinase PACE4; integrin binding; serine proteinase
C; Keywords: duplication; glycoprotein; hydrolase; integrin binding; serine proteinase
F; 1-34 Domain: signal sequence #status predicted <81G>
F; 35-915/Product: probable proproprotein convertase 5 #status predicted <PRO>
F; 17-915/Product: probable proprotein convertase 5 #status experimental <MAT>
F; 164-402/Domain: subtilisin homology <8EP:
F; 173,214,388/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 PDINKCTKCKADCDTCFNKNF--CTKCKSGFYLH--LGKCLDNCPEGLEANNHTMECVSI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 VHCEVSEWNPWSPCTKKGKTC-GFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRK 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PACE4A - mouse (fragment)
C;Species: Mus musculus (bouse mouse)
C;Species: Mus musculus (bouse mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: ISS27
R;Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A;Title: PACE4A is a ubiquitous endoprotease that has similar but not idential. A;Reference number: ISS27
                                                                                                                                                                                                        probable proprotein convertase (EC 3.4.21.-) 5 precursor - rat
N;Alternate names: PC5 precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 ADKKRCRKCAPNCESCFGSHADQCLSCKYGYFLNEETSSCVAQCPEGSYQDIKKNIC---
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A;Residues: 1-912 <RES>
A;Cross-references: GB:D50060; NID:9769700; PIDN:BAA08777.1; PID:9769701
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F;172-410/Pomain: subtilisin homology <SET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%; Score 168; DB 2; Length 915; 26.3%; Pred. No. 0.00075; Live 25; Mismatches 54; Indels
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---TCG 853
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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          :: : |
838 PDSELIRCGECHH-
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Best Local Similarity
Matches 49; Conserva
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A, Molecule type: mRNA
A, Residues: 1-915 < LUS>
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R; Kiefer, M.C.; Tucker, J.B.; Joh, R.; Landsberg, K.B.; Saltman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A; Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A; Reference number: A39490; MUID:92075167; PMID:1741956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A
N;Alternate names: kexin homolog
C;Species: Homo sapiens (man)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038 HIAVID-LAVCLQFCPDGYFENS----RNRTCVP-----CEPNCASCQDHPEYCTSCDHH 1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  737 YFGDTAARRCRR-----CHKGCETCSSRAATQCLSCR-RGFY-----HHQEMNT 779
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A:Rolecule Vrpe: mRNA
A:Residues: 1-1680 cROS>
A:Residues: 1-1680 cROS>
A:Residues: 1-1680 cROS>
A:Cross-references: GB:M94375; NID:g157461; PID:g157462
A:Rote: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
A:Genetics:
A:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HIRLISWIPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:PACE4
A;Cross-references: GDB:131390; CMIM:167405
A;Map position: 15q26-15q26
C;Superfamily: subtilisain-like proteinase PACE4; subtilisin homology
C;Superfamily: subtilisain-like proteinase PACE4 #status proteinase
F;150-969/Product: serine proteinase PACE4 #status predicted <SIG>F;196-434/Domain: subtilisin homology <SBT>F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.6%; Score 176.5; DB 2; Length 1680; Best Local Similarity 28.0%; Pred. No. 0.00033; Matches 60; Conservative 24; Mismatches 77; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 969;
                                                                                                                                                                                                                                                                     A,Cross-references: PlyBase:FBgn0004598
C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;409-652/Domanin: subtilisin homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1178 ECLQNWT-----LNXRDKCIVSGSEGCSESE 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 BIIQHPSAKGNLCPPTNBTRKCTVQRKK-CQKGE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%; Score 173.5; DB 1
28.8%; Pred. No. 0.00034;
tive 16; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ANNHIMBCVSIVHCEVSEWNPWSPCTKKGKTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 28,8%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A39490
A;Molecule type: mRNA
A;Residues: 1-969 <KIE>
A; Accession: A43434
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C. Accession: JC614; "Loguentes, S.; Duke, R.; Franzusoff, A. R. Molf, J.; Pichuantes, S.; Duke, R.; Franzusoff, A. Broc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A.Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1 can also the number: JC6148; MUID:96353880; PMID:875538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C;Comment: This protein functions as a soluble enzyme within the secretory pathway. It
                                                 convertase (EC 3.4.21.-) 5 precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765 GODCOPCHRFCATCAGAGADGCINCTEGYFWEDGRCVQSCSISYYFDHSSENGYKSCKKC 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825 DISCLICINGPGFRONCTSCPSGYLLDLGMCQMGAICKDATRESWARGGPCMLVKKRNLC-- 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGPYLHLGKCLDNCPRGLEAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVS----NPWSPCTKK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 GKTC-----GPKRGTE-----TRVREIIQHPSAKGNLCPPTNETRKCTV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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                                                                                                                                                                                                                                                                                                                   A;Residues: 1-899 <REU>
A;Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C;Genetics:
                                                       gubtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fra
C;Species: Homo sapiens (man)
C;Dete: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C;Accession: GO242
S;Reudelhuber, T.L.
submitted to the EMBL Data Library, Pebruary 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human N;Alternate names: PC6A protease C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C; Esywords: hydrolase; serine proteinase P;148-386/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology C;Ksywords: glycoprotein; hydrolase; serine proteinase P;164-402/Domain: subtilisin homology <SB7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.7%; Score 162; DB 2; Length 899;
Best Local Similarity 22.3%; Pred. No. 0.0018;
Matches 55; Conservative 33; Mismatches 81; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 915;
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ilarity 22.3%; Pred. No. 0.0019;
Conservative 33; Mismatches 81
                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                      A; Reference number: H01242
A; Accession: G02428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 NHTME-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 QRKKCQK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 ORKVI.OQ 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
Les 55; Conserv
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A; Residues: 1-915 <MIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JC6148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
R;Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: CRNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop. A;Reference number: A48225; MUID:93342056; PMID:8341687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Wolecule type: mRNA
A;Residues: 1-915 <1US>
A;Kosidues: 1-915 <1US>
A;Cross-references: 1-915 <1US>
B;L14932; NID:g293327; PIDN:AAA74636.1; PID:g293328
R;Cross-references: T.; Hosaka, M.; Torii, S.; Watanabe, T.; Murakami, K.; Nakayama, K.
J. Biochem. 113, 132-115, 1993
A;Reference number: JX0248; WID:33224489; PMID:8468318
A;Accession: JX0248
A;Accession: JX0248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Cross-references: DDBJ:D12619; NID:g220565; PIDN:BAA02143.1; PID:g220566
A;Note: the authors translated the codon GGC for residue 915 as Ala
C;Superfamily: subtilisin-like proteinase PACER; subtilisin homology
C;Keywords: duplication; 9Jycoprotein; hydrolase; integrin binding; serine proteinase
F;1-34/Domain: signal sequence #status predicted <SIG>F;35-116/Domain: propeptide #status predicted <PRO>F;15-716/Domain: proprotein convertase PC5 #status experimental <PAT>F;117-915/Product: proprotein convertase PC5 #status experimental <PAT>F;164-402/Domain: subtilisin homology <SBT>F;173,214,388/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSCPSGYYGTRYPDINK--CTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 NWHTMB------NPWSPCTK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 NGHDCQPCHRFCATCSGAGADGCINCTEGYVMEBGRCVQSCSVSYYLDHSSEGGYKSCKR 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 KGKTC-----GFKR------GT---ETRVRBIIQHPSAKGNLCPPTNBTRKCF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840 CDNSCLTCNGPGFKNCSSCPSGYLLDLGTCQMGAICKDATEESWAEGGFCMLVKKNNLC- 898
----CHKGCETCTGRSPAQCLSCR-RGFY-----HHQETNT 742
                                                             CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NPCTKCKSGFYLHLGKCLDNCPEGLE 135
                                                                                                  --VSIVHCEVS----EWNPWSPCTKKGKTCGFKRGTETR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GSQNASRGRRQRRMHPNVSQGCQGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 78
                                                                                                                                                                                                                                801 PDSBLVKCGBCHHTCRTCVGPSREBCIHCAKSFHPQDWKCVPACGB-----GP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subtilisin-like proprotein convertase (BC 3.4.21.-) PC5 precursor N;Alternate names: kexin homolog; serine proteinase PC6 C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.0%; Score 167; DB 1; Length 915; Best Local Similarity 23.4%; Pred. No. 0.00088; Matches 58; Conservative 29; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                 177 VREIIGHPSAKGNLCPPTNETRKCTVQRKKCQKGER 212
                                                                                                                                                                                                                                                                                                                                                        ----YPEEMPGL--PHKVCRRCEENCLSCEGSSR 876
      100 YFGDAAARRCRR
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A; Residues: 1-915 <NAK>
                                                                                                                                                                               136 ANNHTMEC
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DD 679 GHYHADK-KRCRKCAPMCESCFGSHGDQCMSCKYGYFLNBETINSCV 723	A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
OY 79 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKOPFCTKCKSGPYLHLGKCLDNCPEGLEAN 137	A;Residues: 1-379 <hsi> A;Cross-references: GB:AF122922; NID:g4585369; PIDN:AAD25402.1; PID:g4585370</hsi>
Db 724 THCPDGSYQDTRKMLCRKCSENCRTCTEFHNCTECRDGLSLQGSRCSVSCEDGRYFN 780	10.5%; Score 158.5; DB 2; Length 379; ilarity 24.9%; Pred. No. 0.0016;
Qy 138 NHTMECVSIVHCEVSEWNPWSPCTKK 163 Db 781 GODCOPCHRECATCAGAGADGCINCTEGYFMEDGRCVOSCSISYPHSSEKGYKSCKKC 940	Matches 60; Conservative 26; Mismatches 72; Indels 83; Gaps 16; Ov 42 COGGCMTCSDYNGCLSCKPRLFPALERIGMKOIGVCLSSC 81
164 GKTCGFKRGTBTRVRBIIQHPSAKGNLCPPTNETRKCTV	182 CPGCRNGGFCNERRICECPDGFHGPHC
DD 841 DISCLTCNGPGFRUCTSCPSGYLLDLGMCQMGAICKDATEESWAEGGFCMLVKRNNLC 898	OY 82 PSGYYGTRYPDINKCTKC-KADCD-TCPNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNH 139
Qy 203 QRKKCQK 209	YGVNCDKANGSTICFNGGTCFYPGKCICPPGLEGB
Db 899 QRKVIQQ 905	Qy 140 TMECVSIVHCEVSEWNFWSPCTKKGKTCGFRRGTETRVREIIQHPSAKGNLCPP 193 Db 272OPCRNGSKCIGKSKKKKSKQGDLCSKFVCEPGCGAHG 318
RESULT 12 T24232	194 -TNETR
hypothetical protein R17.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans	319
C;Mare: 15-OCC-1999 #Bequence_revision 15-OCC-1999 #rext_cnange zi-Jan-Zuou C;Accession: T24232 P:Darlow K	Qy 247 B 247
submitted to the EMBL Data Library, March 1997 A:Reference number: Z19860	Db 374 B 374
A;Accession: T24232 A;Status: preliminary; translated from GB/EMBL/DDBJ	RESULT 14
	I53282 gene PACB4 protein - rat
A;Cross-references: EMBL:Z92809; PIDN:CAB07269.1; GSPDB:GN00021; CESP:R17.3 A;Experimental source: clone R17	C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C;Genetics: A;Gene: CES:R17.3	C;Accession: 153282 R;Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.E. Endominalog: 125 1170-116 1004
Ajnap position: 3 Ajintrons: 36/3; 89/3; 179/2; 241/1; 306/1; 346/2 Gjsuperfamily: Caenorhabditis elegans hypothetical protein R17.3	AUGOCILUACOLY 159, 170-1109, 157-8. AjTitle = subtilisin-like endoprotease prevalent in the anterior pituitary and r AjReference number: 153282; MUID:94349873; PMID:8070361
.6%; Score 161; DB 2;	A; Accession: 153282 A; Status: preliminary; translated from GB/EMBL/DDBJ
red. No.	A;FOLECULE LYDE: MACH. A;Roadunes: CRES.> A:Crosd-reference: GR:131894: NID:c496221: PIDN:AAA61987.1: PID:c496222
QY S9 KPRLPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSG 118	C;Genetics: A;Gene: PAGEn: PAGEN: whilisin-like proteinase PAGEN: subtilisin homology
116 OVIII CACA NAVADANI DANAMINADANI LILIBANI LILBANI	Fil77-415/Domain: subtilisin homology <sbt></sbt>
	Query Match 10.3%; Score 156.5; DB 2; Length 937; Best Local Similarity 23.6%; Pred. No. 0.0043; Marches 51: Conservative 24: Mismatches 80: Indels 61: Gaps 11:
OY 179 BIIOHPSAKGALCPPTWETRKCTVQRKKCQKGERGKKGRERKRKKDNKGESKRAIPDSKS 238	19 YIGSQUARRERPHPNVSQCQCGCATCSDVNGCLSCKPRLPFALERIGMKQIGV 7
2/2 BYLQHADAQARAÇEFUNDINIYÇYD	grsprociscr-kgr
OY 239 LESSABLEDVENKOOLANAKAVODANASASASASASASASASASASASASASASASASASASA	Qy 77 CLSSCPSGYYGTRYPDINKCTKCKADCPTCPNR-NPCTKCKSGPYLHLGKCLDNCPRGLE 135
RESULT 13 A59180 Wat inhipitory factor-1 - human	QY 136 ANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETR 176 :::
C;Species: Homo sapiens (man) C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000	177
C;Accession: A59180 R;HBieh, J.C.; Kodjabachian, L.; Rebbert, M.L.; Rattner, A.; Smallwood, P.M.; Samos, C.E Narura 198 431-434 1999	Db 854YPEEMPGLPHKVCRRCDENCLSCEGSSR 881
Nature 59, 131-1970, 1379, 1379 Affitte 5 A new Secreted protein that binds to Wmt proteins and inhibits their activities A;Reference number: A59180; MUID:99215557; PMID:10201374 A;Accession: A59180	RESULT 15 A47723

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F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C;Accession A7723
R;Ruiz i Alteaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Bcropic neural expression of a floor plate marker in frog embryos injected with A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Status: preliminary
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A;Residues: 1-803 <RUI.
A;Cross-references: GB:L09123; NID:g409244; PIDN:AAA19105.1; PID:g409245
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>
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Isold=Q04592-1; Sequence=VSP 005438, VSP 005439;
Isold=Q04592-2; Sequence=VSP 005438, VSP 0054439;
Isold=Q04592-2; Sequence=VSP 005438, VSP 0054439;
Isold=Q04592-2; Sequence=VSP 005438, VSP 0054439;
Interse edveloping nervous system, the ribs and the liver, but markedly upregulated at discrete sites during development. At ES.5, prominent expression in extrembly pronic endoderm, and on and nascent mesoderm. At ES.5, abundant expression in somites and yolk sac followed by a confination to dermamyotome compartment. Between ES.5 and ES.1.5, abundant expression in the limbs is confined to the condensing mesenchym surrounding the cartilage. At this stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the tongue. At ES.5, abundant expression in petchelial cells of the intestinal villi. Isoform A is most abundant at all stages but significant levels of isoform B occur at ES.2.5.
Isold-Common and in the muscle as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                       MEDLINE=97436919; PubMed=9291583;

MEDLINE=97436919; PubMed=9291583;

Rancourt S.L., Rancourt D.E.;

"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";

"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";

Dev. Genet. 21:75-81(1997).

"In plantation, likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.

C.I. CMTALYIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-ARG-I-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

C.I. SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PCSB IS A TYPB I MEMBRANE PROTEIN LOCALIZED TO SECRETORY PATHWAY. PCSB IS A TYPB I MEMBRANE PROTEIN WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropen Bloinformatics institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
SIMILARITY: Belongs to peptidase family $8.
SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bvent=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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InterPro; IPR009030; Grow_fac_recep.
Cell Biol. 134:181-191(1996)
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EMBL; D12619; BAA02143.1; -.
EMBL; L14932; AAA74636.1; -.
PIR; A48225; A48225.
PIR; S34583; S34583.
HSSP; Q99405; IMPT.
MEROPS; S08.076; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٨
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CPPT--NBTRKCTVQRKKCQKGBRGKKGRERKRKKPNKGBSKEAIPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rydrolase, Serine protease, Glycoprotein, Zymogen, Signal;
Cleavage on pair of basic residues, Repeat; Alternative splicing;
Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLEAVAGE (AUTO-) (BY SIMILARITY)
CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EC850E2DF20EA1C3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
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(BY
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N-LINKED (GLCWAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (in isoform PCSA)
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N-LINKED
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InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002804; Peptidase_S8B.
InterPro; IPR002020; Protease_Inhib-Pfam; PP00183; P_proprotein; I.
Pfam; PP000182; Peptidase_S8; I.
PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; I.
SNART; SM00261; FU; Z2.
PR0SITE; PS00136; SUBTILASE_ASP; I.
PROSITE; PS00138; SUBTILASE_HIS; I.
PROSITE; PS00138; SUBTILASE_ERS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
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RESULT 3
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                                                                                                                                                                                                                                                                          MEDLINE-20175281; PubMed=10708868;

MEDLINE-20175281; PubMed=10708868;

A Diva A.A. Jr., Chan S.J., Steiner D.F.;

"Evolution of the protochordate amphioxus.";

Thomologue of PC6 in the protochordate amphioxus.";

Biochim. Biophys. Acta 1477:338-348(2000).

"Ithin the constitutive and regulated endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(R/R)R consensus motif (By similarity).

"Ithin the constitutive and regulated secretory pathway. Capable of cleavage at the RX(R/R)R consensus motif (By similarity).

"Ithin the constitutive and regulated secretory pathway. Capable of cleavage of mature proteins from their protochins by cleavage of Arga-Yaa-'asa-ARG-|-zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

"ISOPORM BIS A TYPE I MEMBRANE PROTEIN.
                                                                                   PCK5 BRACL STANDARD; PRT; 1696 AA.
Q9NJ15; Q9NJ14; Q9NJ16;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9NJ15-3; Sequence=VSP 005442, VSP 005443; DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                        Branchiostoma californiensis (California lancelet) (Amphioxus).
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9NJ15-2; Sequence=VSP_005444, VSP_005445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to peptidase family S8. SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR002084; Peptidase S8.
InterPro; IPR002884; Peptidase S8.
InterPro; IPR009020; Protease Inhib.
Pfam; PF00483; Peptidase S8; 1.
Pfam; PF00042; Peptidase S8; 1.
PRMYS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; 1.
SWART; SW00261; FU; 17.
PROSITE; PS00137; SUBTILASE ASP; FALSE NEG.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9NJ15-1; Sequence=Displayed;
                                                                                                                                                                           (Proprotein convertase PC6-like) (aPC6).
EMBL; AF184615; AAF26300.1; -. EMBL; AF184616; AAF26301.1; -. EMBL; AF184617; AAF26302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q99405; IMPT.
                                                                                                                                                                                                                                       Branchiostoma.
NCBI_TaxID=7738;
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13;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
DITILIDRGECTISCOPPERMORREKKCNACHPICKECSDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDTCTACNDGFILIDASSCEAGCP -> AENQNQASFCPFA
PREVSVIABIALGHIRYSLIDVPPQSNSPPDTVLGADRARL
TTATSAAGRCA (in isoform C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP_005443.
CHPTAGESDEYDFTACHORPLLTDASSCEAGCPPGQFL
HHGDDSGFREGTTC -> IARCVDRRDRSWCDLVLRFNPC
VRRYFVKRCCGTCKLVMEDRPMRRGSSQPTQGRN (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 184.5; DB 1; Length 1696;
; Pred. No. 8.2e-06;
25; Mismatches 74; Indels 119; Gaps
                                                                                                                                                                   POTENTIAL.
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
Cleavage on pair of basic residues; Repeat; Alternative splicing;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P30432; Q24301;
01-APR-1993 (Rel. 25, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Purin-like protease 2 precursor (BC 3.4.21.75) (Furin 2).
PURZ OR CG187734/CG4235.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYS-RICH MOTIP (CRM) REGION.
CLEAVAGE (AUTO-) (RV CTATTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1344 1696 Missing (In isoform A).
/FTIG-VSP 005445.
1696 AA; 188410 MW; 281CBE1784257CBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1559 BAPYGYHAMKHLCTACCEEGSPENEYCCICHESTRLCITDRE 1600
                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP 005442.
Missing (in isoform C).
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1 Similarity 22.7%;
64; Conservative 2!
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AMEMINGENETREY;

Addams M.D. Celnikter S. B., Holl R.A., Brans C.A., Gocayne J.D.,

Addams M.D. Celnikter S. B., Holl R.A., Brans C.A., Gocayne J.D.,

R. Addams M.D. Celnikter S. B., Li P.W., Hoskins R.A., Galle R.F.,

R. Sutton G.G., Wortean J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

R. Bandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

R. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

R. Benceson K.Y. Bencos P.V., Berman B.P., Bandari D., Bolabakov S.,

R. Borkova D., Botchen M.R., Bouck J., Broketein P., Barchter P.,

R. Buris K.C., Busam D.A., Buller H., Cadleu B., Center A., Chanfra I.,

R. Buris K.C., Gabriellan R.B., Gard. R.D., Dew I., Diavies P.,

R. Durbin K.J., Bvongelista C.C., Ferraz C., Ferriers S., Plaischmann W.,

R. Baloson K., Doup L.B., Downes W., Dogan-Rocha S., Punkov B.C., Dunn P.,

R. Durbin K.J., Bavagelista C.C., Ferraz C., Ferriers S., Plaischmann W.,

R. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

Alali M., Kalush P., Karpen G.H., Ke Z., Kannison J.A., Kechunison J.A., Kechunison J.A., Kechunison J.A., Kechunison J.A., Kechunison J.A., Kechunison D.L.,

R. Minnel B.E., Kodiars C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liasko P., Lei Y., Levitekh A.A., Li J.H., Li Z., Liang Y., Lin X.,

R. Martel B.W., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,

R. Nelson D.R., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,

R. Syliekas R., Teccor C., Turner K., Venter E., Wand A., Rang X.H.,

R. Syliekas R., Moodage T., Wohley K., Wu D., Yang S., Yan Q.,

R. Millams S.M., Woodage T., Wohley K., Wu D., Yang S., Zhu Y., Smith H.O.,

R. The genome sequence of Drosophila melanogaster F., Suhnyarian S., Smith R., Stone E., Stunker S., Stone C. St., Stone S
                                                                                                                                          SECUENCE FROM N.A.
STRAIR=Oregon.R. Tuebingen, and Iso-1;
MEDLINE=92381036; PubMed=1512259;
MEDLINE=92381036; PubMed=1512259;
Roebroek A.J.W., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
"Cloning and functional expression of Dfurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with multiple
repeats of a cystein motif.";
J. Biol. Chem. 267:17208-17215(1992).

    FUNCTION: Furin is likely to represent the ubiquitous endoprotease
activity within constitutive secretory pathways and capable of
cleavage at the RX(K/R)R consensus motif (By similarity).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Dfur2 gene of Drosophila melanogaster: genetic organization, expression during embryogenesis, and pro-protein processing activity of its translational product Dfurin2."; DNA Cell Biol. 14:223-234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ISO-1;
MRDILINE=95186066; PubMed=7880443;
Roebroek A.J.W., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L., van de Ven W.J.M.;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Kaa-Yaa-Arg-1-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their

respective precursors. TISSUE SPECIFICITY: Transient expression in a subset of central

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nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                        development.
--- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
--- SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
, CYS-RICH.
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PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
HYDOTOLASE; SETINE PTOCEASE; Glycoprotein; Signal; Transmembrane; Multigene family; Zymogen; Repeat.
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3F9E749F0B021CF6 CRC64;
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CYTOPLASMIC (POTENTIAL)
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FURIN-LIKE PROTEASE
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InterPro; IPR005212; Furin repeat.
InterPro; IPR0019030; Grow Fac. recep.
InterPro; IPR001908; Peptidase SB.
InterPro; IPR0019884; Peptidase SB.
InterPro; IPR0019884; Peptidase SB.
InterPro; IPR0019020; Protease Inhib.
Ffam; PF00182; Peptidase SB; 1.
Pfam; PF00182; Peptidase SB; 1.
PRNNTS; PR00712; Peptidase SB; 1.
SNART; SN00117; Peptidase SB; 1.
SNART; SN00117; Peptidase SB; 1.
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EMBL; L33831; AAA69660.1; -.
EMBL; AR003502; AAR48598.1; -
PIR; A43434; A4344.
HSSP; Q99405; 1MPT.
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MBROPS; 808.049; -.
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CONFLICT
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                                                                                                                                         120 YLHLGKCLLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 178
                                                                                          62 IPPALERICAKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCP--NKNPCTKCKSGF 119
                                                61
                                               3 HLRLISWLPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                          Gaps
                                                                                                                                                                                                                                                                 PAC4 HUMAN STANDARD; PRT; 969 AA.
P29122; Q15099; Q15100; Q9UEG7; Q9UEJ1; Q9UEJ2; Q9UEJ7; Q9UEJ8; Q9UEJ2; Q9UEJ7; Q9UEJ8; Q9UEJ9; Q9VEG9; Q1-DRC-1992 (Rel. 24, Created)
01-DRC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 31, Last annotation update)
Paired basic amino acid Cleaving enzyme 4 precursor (RC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
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                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A., Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a second human subtilisin-like protease gene
                         53,
  Length 1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOPORMS PACE4A-I AND PACE4B).
TISSUE=Hepetoma, and Kidney.
MEDLINE=22075167; PubMed=1741956;
Kiefer M.C., Tucker J.B., Joh R., Landsberg K.B., Saltman D.,
 11.6%; Score 176.5; DB 1; Length 28.0%; Pred. No. 3e-05; ive 24; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a novel PACB4 isoform, PACB4B.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 204:1381-1382(1994)
DB 1;
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                                                                                                                                                                                                            1177 ECLONWI -----LNKRDKCIVSGSEGCSESE 1202
                                                                                                                                                                                       179 EIIQHPSAKGNLCPPTNETRKCTVQRKK-CQKGR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94235049; PubMed=8179631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95071480; PubMed=7980617;
                        60; Conservative
                                                                                                                                                                                                                                                                                                                                                                 convertase 4) (SPC4)
PACE4.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PACE4 isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PACE4 isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Magahama M., Taniguchi T., Hashimoto B., Imamaki A., Mori K.,
Magahama M., Taniguchi T., Hashimoto B., Imamaki A., Mori K.,
Tsuji A., Matsuda Y.;
Tsuji A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whereas mature PACB4. I exists only as a monomer, suggesting that propeptide cleavage affects its tertiary or quaternary structure. SUBCELLULAR LOCATION: PACB4A. I and PACB4-All are secreted. PACB4C and PACB4CS are not secreted and remain probably in zymogen form in endoplasmic reticulum. PACB4B. I and PACB4B. I are retained transcribed by through a hydrophobic cluster in their C-terminus. PACB4B might be secreted.
MEDLINE-97335942; PubMed-9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
A novel human PACE4 isoform, PACE4B is an active processing protease
containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
Bando M., Sakai B., Mori K., Akamatsu T., Matsuda Y.;
"Genomic organization and alternative splicing of human PACE4 (SPC4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mochring T.J.;
"Randoprotease PACR4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain.";
Biochem. J. 339:639-647(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=P29122-6; Sequence=VSP 005427, VSP_005434, VSP_005435;
Note=Probably enzymatically inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOPORMS PACE4A-I; PACE4A-II; PACE4CS; PACE4D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G., "Punctional analysis of human PACE4-A and PACE4-C isoforms: identification of a new PACE4-CS isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99233559; PubMed-10215603;
Sucic J.F., Mochring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSP_005429;
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Note=Probably enzymatically inactive;
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Name=PACE4A-1; Synonyms=PACE4;
IsoId=P29122-1; Sequence=Displayed;
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IsoId=P29122-3; Sequence=VSP 005428,
Note=Probably enzymatically Inactive;
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MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kexin-like processing endoprotease.";
J. Biochem. 122:438-452(1997).
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MEDLINE=98021085; PubMed=9378725;
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Local Similarity
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Matches 44
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                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           Name=PACE4B-II;
IsoId=P29122-8; Sequence=VSP 005436, VSP 005437;
IsoId=P29122-8; Sequence=VSP 005436, VSP 005437;
TISSIGE SPECIPICITY: Bach PACE4-isoform exhibits a unique
placenta, lung, skeletal muscle, kidney, pancreas, but at
comparatively higher levels in the liver. PACE4A-II is at least
expressed in placenta. PACE4B was only found in the embryonic
expressed in placenta. PACE4B was isolated. PACE4C and PACE4D
expressed in placenta. PACE4B-II is expressed in cerebellum,
placenta and pituitary. PACE4B-II is at least present in
                                                                                                                                                                                         -1- DOWAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic reticulum. Isoform PACB4D lacks the propeptide domain.
-1- SIMILARITY: Belongs to peptidase family S8.
-1- SIMILARITY: Contains 1 PLAC domain.
Name=PACE4B-1;
IsoId=P29122-7; Sequence=VSP_005437;
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737 YPGDTAARRCRR-----CHKGCBTCSSRAATQCLSCR-RGFY----HHQEMYT 779
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780 CVILCPAGFYADE--SQKNCLKCHPSCKKCVDBPBKCTVCKBGFSLARGSCIPDCBPGTY 837
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Dev. Biol. 181:268-283(1997).

-I- FUNCTION: Likely to represent a widespread endoprotease activity

-i- FUNCTION: Likely to represent a widespread endoprotease activity

within the constitutive and regulated secretory pathway. Capable

of cleavage at the RX(K/R)R consensus motif. May be responsible

for the maturation of gastrointestinal peptides. May be involved

in the cellular proliferation of adrenal cortex via the activation

of growth factors.

-i- CATALYTIC ACTIVITY: Release of mature proteins from their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and peripheral tissues of
th other proprotein
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1D PCK5 RAT

STANDARD; PRT; 1877 AA.

1D PCK5 RAT

C 1413; Q62914;

DT 01-NOV-1995 (Rel. 32, Created)

DT 15-MAR-2004 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DF Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)

DB (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)

C 17-55 (PC6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE=20214819; PubMed=10749928; Xiang Y., Molloy S.S., Thomas L., Thomas G.; Thomas G.; Thomas C., Thomas G.; Thomas C., Thomas G.; Thomas C. Complements that direct of Schoolplasmic domain concains two acidic clusters that direct sorting to distinct trans-Golgi network/endosomal compartments."; Mol. Biol. Cell 11:1257-1273 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Adrenal gland;
MEDLINE=93342056; PubMed=8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Adrenal gland;
De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                          Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                              DB 1;
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Zheng M., Seidah N.G., Pintar J.B.;
"The decopmental expression in the rat CNS an
professes PCS and PACE4 mRNAs: comparison with
                                                                                                                                                                                              11.4%; Score 173.5; DB 1
28.8%; Pred. No. 2.9e-05;
tive 16; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       838 PDSELIRCGECHH--------TCG 853
EMBL; AB001901; BAA21624.1; JOINED.
EMBL; AB001902; BAA21624.1; JOINED.
EMBL; AB001903; BAA21624.1; JOINED.
EMBL; AB001904; BAA21624.1; JOINED.
                                                                                                                                                                                                                                                                            44; Conservative
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Name=PCSB; Synonyms=Long;
Name=PCSB; Synonyms=Long;
Isold=P41413-1; Sequence=Displayed;
Name=PCSB; Synonyms=Long;
Isold=P41413-2; Sequence=USP 005440, VSP 005441;
Isold=P41413-2; Sequence=VSP 005440, VSP 005441;
Isold=P41413-2; Sequence=VSP 005440, VSP 005441;
Isold=P41413-2; Sequence=VSP 005440, VSP 005441;
Isold=PGSUS SPECIFCITY: Expressed in the integrin. brain adrenal gland, anterior pitultary, thyroid, ovaries, testis and lung. Highest levels are found in the gut, duodenum, jejunum and ileum. Expression is higher in female than in male reproductive organs.
Isold=PGELOPMENTAL STAGE: First detected at E9 in highly restricted regions of the neural tube, in caudal myotomes, and at the materno-embryonic junction of the uterus. At E10, restricted expression is detected in the optic and obtic vesicles, the roof of midbrain, and trunk myotomes. By midgestation (E13-E16), expression in the developing nervous system has expanded to multiple regions including hippocampus, thalamus, hypothalamus, brain stem, and spinal cord. Expression is also detected in several peripheral organ systems, including gut, lung, adrenal and kydney primordia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
proproceins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
-!- SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R InterPro; IPR006212; Purin repeat.
R InterPro; IPR00289; Peptidase_S8.
InterPro; IPR00289; Peptidase_S8.
R InterPro; IPR00280; Peptidase_S8.
R InterPro; IPR002020; Procease_Inhib.
R Fan, PF01483; Purproctein; I.
R Probom; PD000717; P_domain; I.
R MART; SM00261; FU; 6.
R PROSITE; PS00136; SUBTILASE_ASP; I.
R PROSITE; PS00137; SUBTILASE_RIS; I.
R PROSITE; PS00139; SUBTILASE_SR; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CATALYTIC.
HOMO B.
CYS-RICH MOTIF (CRM) REGION.
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                                                                                                                                                         Bvent=Alternative splicing, Named isoforms=2,
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE 5
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116
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HSSP; Q99405; IMPT.
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 VHCEVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 ------GKCSENCKTCTGFHNCTR------CKGGL---SLQGSRCSV--- 771
                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCK5 HUMAN STANDARD; PRT; 913 AA.
Q92824; Q13527;
16-CCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR------ICVSSCPPGHP---H
                                                                                                                                                                                                                                                                                                                                                                                       36 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                            58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; "Isolation of the human PCG gene encoding the putative host protease for HIV-1 gp160 processing in CD4+ T lymphocytes."; Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                  ATERSWAEGGPCMLVKKNNLCQRKVLQQLCCKTCTPQG
                                                     CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                             11.1%; Score 168; DB 1; Length 1877; 26.3%; Pred. No. 0.00014; ive 25; Mismatches 54; Indels 58
                                                                                                                                                                                                                                                                      Missing (In isoform PC5A).
/FTId=VSP 005441.
MW; 890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Franzusoff A., Miranda L., Wolf J., Pichuantes S., Lu Y.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
AC 1.
AC 2.
CLEAVAGE (AUTO-) (BY S.
CELL ATTACHMENT SITE (
CHARGE RELAY SYSTEM (B
CHARGE RELAY SYSTEM (B
CHARGE RELAY SYSTEM (B
                                                                                                                                                                                                                                              (in isoform PC5A)
/Frid=VSP 005440.
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MEDLINE=96353880; PubMed=8755538;
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                                                                                                                                                                                                                                                                                                                                             Local Similarity 26.3
 1844
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MERCOPS: SUB-076; -.

MERCOPS: SUB-076; -.

MIM; 600488; -. C:extracellular space; TAS.

MIM; 6000452; F:serine-type endopepidase activity; TAS.

GO; GO:0005263; P:serine-type endopepidase activity; TAS.

GO; GO:0005269; P:peridase Sub.

MIR: FROOD TEPPO; PERO00209; Peptidase Sub.

InterPro; PER000209; Peptidase Sub.

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IsoId=Q92824-1; Sequence=Displayed; IsSUE SPECIFICITY: Expressed in T-lymphocytes. DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
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CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
-!- SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                  Comment=2 isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC.
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79 SSCPSG-YYGTRYPDINKCTKCKADCDICPNRNPCTKCKSGPYLHLGKCLDNCPEGLEAN 137
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A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausperg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownerein M.J., Usdin T.B., Tobhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachey J., Helton B., Ketteman M., Madan A., Kodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Racheley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                 21 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99215557; PubMed=10201374;
Hsieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.,
Ranilwood P.M., Photein that binds to Wnt proteins and inhibits their
                                                                                                                                                                                                                                                                            78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                      10.7%; Score 162; DB 1; Length 913; 22.3%; Pred. No. 0.00018; ive 33; Mismatches 81; Indels "
                                                 118 S -> F (IN RBF. 3).
121 V -> A (IN RBF. 3).
131 R -> A (IN RBF. 3).
131 R -> A (IN RBF. 3).
101775 MW; 21389264CAD7546C CRC64;
  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0915W5; Q8WVG4;
16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Wht inhibitory factor 1 precursor (WIF-1).
                            (GLCNAC
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N-LINKED
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Nature 398:431-436(1999).
                                                                                                                                                                                                                                                                               55; Conservative
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  802
852
118
121
511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         897 QRKVLQQ 903
  802
852
118
121
511
511
601
613 AA;
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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                                                                                                          82 PSGYYGTRYPDINKCTKC-KADCD-TCFNKNPCTKCKSGPYLHLGKCLDNCPEGLEANNH 139
                                                                                                                                                                                                                140 TMECVSIVECEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPP---- 193
                                                                                                                                                                                                                                                    CZISKCP--QPCRNGGKCIG---KSKCKCSKGYQGDLCSKPVCEPGCGAHG 318
                                                                                                                                                                                                                                                                                                                           194 -TNETRKCTVQRKKCQKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKEIP 246
                                                                                                                                                                                                                                                                                                                                                          182 CPGGCRNGGPCNERRICECPDGFHGPHCEKALCTPRCMNG------GLCVTPGFCIC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 398.431-436 (1999).

-I- FUNCTION: Binds to WNT proteins and inhibits their activities. May be involved in mesoderm segmentation.

-I- SUBCELLULAR LOCATION: Scretced.

-I- TISSUB SPECIFICITY: During somatogenesis, expressed predominantly in unsegmented paraxial presomitic mesoderm and, to a much lesser extent, in newly segmented somites.

-I- DEVELOPMENTAL STAGE: First expressed at neurula stages.

-I- SIMILARITY: Contains 1 WIF domains.
                                                                                                                                            233 PPGFYG------VNCDKANCSTTCFNGGTC------PY--PGKCI--CPPGLEGE--
  COGGCAT---CSDYNGC------LSCKPRLFPALERIGMKOIGVCLSS----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=9921557; PubMed=10201374;
Hisleh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;
"A new secreted protein that binds to Wnt proteins and inhibits their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
WNT inhibitory factor 1 precursor (WIP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00740; IEDM.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR00249; Laminin_EGF.
InterPro; IPR003306; WIF.
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Pfam; PF02019; WIF; 1.
PRINTS; PR00011; BGPLAMININ.
SWART; SMO018; BGF; 4.
SWART; SMO0469; WIF; 1.
PROSITE; PS00022; BGF_1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                        E 247
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ID WIFL XENLA
AC Q9W6F8;
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                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds to WNT proteins and inhibits their activities. May be involved in mesoderm segmentation.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: B EBF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prant Prototols BEST: S.
Prant Prototols BEST: S.
Prant Prototols BEST: 1.
PRINTS: PROTOTI BESTIANININ.
SMART: SMOOLS: BEST 1.5
SWART: SMOOLS: BEST 1.5
PROSITE: PSOOLS: BEST 1.5
PROSITE: PSOOLS: BEST 2.5
PROSITE: PSOOLS: BEST 
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Q -> L (IN REF. 1).
32RC54D60529EP96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNT INHIBITORY FACTOR 1. WIF.
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BGP-LIKB 2.
BGP-LIKB 3.
BGP-LIKB 4.
BGP-LIKE 5.
POTENTIAL.
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InterPro; IPR006210; IEGF.
InterPro; IPR002049; Laminin_EGP.
InterPro; IPR003306; WIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF122922; AAD25402.1; -. EMBL; BC018037; AAH18037.1; -.
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178
379 AA;
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tes 60; Conserv
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262
273
278
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DOWAIN
DOWAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 YIGSONASRGRRORRMHPNVSQGCQGGCATCSDYN--GCLSCKPRLPPALBRIGMKQIGV
                 pitultary and regulated by thyroid status.",
Endocrinology 135:1178-1185(1994).
--- FUNCTION: Likely to represent an endoprotease activity within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAIRED BASIC AMINO ACID CLEAVING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium; Cleavage on pair of basic residues; Repeat.
SIGNAL 1 45 POTENTIAL.
PROPEP 46 132 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (AUTO-).
CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
    "PACE4: a subtilisin-like endoprotease prevalent in the anterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
:csc7C33705C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%; Score 156.5; DB 1; Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO B.
CYS-RICH MOTIF (CRM) REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104053 MW; P3865557C33705C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 0.00046; 24; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC.
                                                                                                                                                                                                                                              -i-SIMILARITY: Belongs to peptidase family $8.-i-SIMILARITY: Contains 1 homo B/P domain.-i-SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006212; Purin repeat.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR002002; Protease_Inhib.
Pfam; PP01082; Peptidase_S8; 1.
Pfam; PP00082; Peptidase_S8; 1.
ProDom; PR000712; PermILISIN.
ProDom; P0000717; Permain; 1.
SMART; SM00261; FU; 5.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_ASP; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L31894; AAA61987.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 23.6%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
536
186
227
401
240
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; 153282; 153282.
HSSP; Q99405; 1MPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                882
900
937 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S08.075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 PSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEANNHTM 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQGGCAT---CSDYNGC-----LSCKPRLFFALERICMKQIGVC---LSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGYYGINCDKVNCTTHC-LNGGTCP------YPGKCI--CPSGYBGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 ECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: || | | :: | | : : | 316 IEPNKCQCKE-GWNGRYCNKKYGSNLAMALRPTGSRNRQHTPSPKRTEDRQALPE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein convertase 4) (SPC4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 VQRKKCQKGERGKKGRERKRK-----KPNKGESKEAIPDSKSLESSKEIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71;
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.4%; Score 157.5; DB 1; Length 374; 24.3%; Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUR=Hypothalamus, and Pituitary;
MEDLINE=94349873; PubMed=8070361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Indels
                                    , WIF; 1. domain; Signal; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           41071 MW; B26F973B0F00ACF8 CRC64;
                                                                                            WIT INHIBITORY FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          937 AA
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BGF-LIKE 2.
BGF-LIKE 3.
EGF-LIKE 4.
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PROSITE; PS50026; EGF_3; 4. PROSITE; PS50026; EGF_3; 4. Repeat; EGF-like domain: Sivent etc.
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                                                                Whit signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 AA;
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063415;
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CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 135
                853
                                                                                   806 PDSELIRCGECHHTCRTCVGPSREECIHCAKSPHFQDWKCVPACGE-----GF-----
                                                        ----VSIVHCEVS----EWNPWSPCTKKGKTCGFKRGTETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Bctopic neural expression of a floor plate marker in frog embryos injected with the midline transcription factor Pintallavis.", Proc. Natl. Acad. Sci. U.S.A. 90:8266-8272(1993).
-1-FUNCTION: Promotes the attachment of spinal cord and sensory neuron cells and the outgrowth of neurites in vitro. May contribute to the growth and guidance of axons in both the spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cord and the PNS.
SUBCELLUAR LOCATION: Secreted.
SUBCELLUAR LOCATION: Secreted at high levels in the floor plate.
SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL) .
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                              177 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 212
                                                                                                                                           ----YPEEMPGL --PHKVCRRCDENCLSCEGSSR 881
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 156; DB 1;
Pred. No. 0.00044;
                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion.
                                                                                                                                                                                                                      803 AA
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TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Embryo;
MEDLINE-93376785; PubMed-8367492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002861; Reeler.
InterPro; IPR000884; TSP1.
Pfam; PP02014; Reeler; 1.
Pfam; PR00099; tsp 1; 6.
SMART; SM0209; TSP1; 6.
PROSITE, PS0092; TSP1; 6.
Glycoprotein; Signal; Repeat; ISP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90702 MW;
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24.6%;
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                                                                                                                                                                                                                    STANDARD;
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489
549
605
662
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210
677
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                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                             P-spondin precursor.
                                                        136 ANNHTMEC--
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Best Local Similarity
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CARBOHYD
CARBOHYD
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                                       38 VSQGCQGGCATCSDYNGCLSCKPRLFFALRRIGMKQIGVCLSSCPS--GYYGTRYPDINK
                                                                                                           96 C--TKCK------ADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEANN---
                                                                                                                                                                                     139 -HTMECVSIVHCEVSEMNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPPTWET
                                                                        544 VNEECEPSSCIVTEWAEWEECS----ATCRMGMKKRHRMIKMTPADGSMCKADTTEVEK
                                                                                                                                                                                                                                                                                     and adult
 Gapa
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                                                                                                                                                                                                                                                                                                                                                                                          NTC2 MOUSE STANDARD; PRT; 2470 AA.
035516; Q06008; Q60941;
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.,
Tsujimoto Y.;
"Mutation in ankyrin repeats of the mouse Notch2 gene induces early
embryonic lethality.";
Development 126:3415-3424(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamada Y., Higuchi M., Tsujimoto Y.;
Complete amino acid sequence and mutliform transcripts encoded by
single copy of mouse Notch2 gene.";
Submitted (JUL-1934) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1765-2153 FROM N.A.
MEDLINE-97075110; PubMed-8917536;
Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                               RKCTVQRKKCOKGERGKKGRERKRKKPNKGESKEA I PDSKSLESSKE I PEQRENKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lardelli M., Lendahl U.; Motch bomologues coexpressed in "Motch A and Motch B-two mouse Notch homologues coexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
MEDLINE=5933833, PubMed=760514;
Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.;
"Differential expression of Notchl and Notch2 in developing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
MEDLINE=21523956; PubMed=11518718;
 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin D.I.;
"Inhibition of granulocytic differentiation by mNo
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse brain.";
Brain Res. Mol. Brain Res. 29:263-272(1995)
 35, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 316-1518 FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
MEDLINE=93178563; PubMed=8440332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99396706; PubMed=10393120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wide variety of tissues.";
Exp. Cell Res. 204:364-372(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6; TISSUE=Thymus;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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not heart.
--- DBVELOPHENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.
--- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proceolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(TM) and a N-terminal fragment N(TM) and binding, it is cleaved by TWP-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch-derived peptide containing the intracellular domain (NECD) from the membrane.
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                                                                                                                                                                                                                                                                                                                                                               POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF WET-1699.

WEDLINE=21374376; PubMed=11459941;
Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
"Conservation of the blochemical mechanisms of signal transduction among mammalian Notch family members.";

"Conservation of the blochemical mechanisms of signal transduction and anogenian Notch family members.";

"In Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"In Proc. Natl. Acad. Or Sci. U.S.A. 98:9026-9031(2001).

"In Proc. Natl. Acad. Sci. U.S.A. 98:9026-903.

"In Proc. Natl. Acad. Sci. U.S.A. 98:9026-903.

"In Proc. Natl. Acad. Sci. U.S.A. 90:9026-903.

"In Proc. Natl. Acad. Sci. U.S.A. 90:9026-903.

"In Proc. Natl. Acad. Sci. U.S.A. 90:9026-903.
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SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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EMBL; X68279; CAA48340.1; -.
EMBL; X68279; CAA48340.1; -.
EMBL; U31881; AA52524.1; -.
EMBL; U31881; AA5175, A49175, A4917
Saxena M.T., Schroeter B.H., Mumm J.S., Kopan R.; "Murine notch homologs (N1-4) undergo presenilin-dependent
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-i- SIMILARITY: Belongs to the NOTCH family.
-i- SIMILARITY: Contains 35 BGP-like domains.
-i- SIMILARITY: Contains 2 Lin/Notch repeats.
-i- SIMILARITY: Contains 6 ANK repeats.
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                                                                                                                                                                           proteolysis.";
J. Biol. Chem. 276:40268-40273(2001)
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                                                                                                                                                 983 ENNIDECTE----SSCFNGGTCVDGINSPSCLCPVGFTGPFCLHDINECSSNPCLNAGT 1037
                                                                                                                                                                                     945 QTDMNECLSEPCKNG-GTCSDYVNSYTC------TCPAGFIGVHC 982
                                                                                                                                                                       126 CLDN------CPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGFKRGTETRV 177
                                                                                                                          91 P-DINKCTKCKADCDTCFNKNFC------125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYCOSINE PROSPACE.
SUBUNIT: TERRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOWAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOWAIN. SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F
                                                                              31 ORRMHPNVSQGCQGCCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                        53; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du J., Delafontaine P.;
"Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor CDNA."; circ. Res. 76:963-972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 187:934-939(1992).
-1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF WITH A HIGH APPINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leroith D., _{\rm I} "Developmental regulation of the rat insulin-like growth factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor I receptor precursor (BC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 913-1017 FROM N.A.
MEDLINE=92412145; PubMed=1530648;
Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
Furachi H., The insulin receptor family, insulin receptor-related receptor, is expressed preferentially in the
                                  DB 1; Length 2470;
                                                                                                                                                                                                                                          1077 ---VQEKARPHCLCPPGWDGAYCDVLNVSCKAAALQKG 1111
                                                                                                                                                                                                                     178 REIIQHPSAKGNLCPPTNETRKCTVQRKKC----QKG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
                                ch 9.9%; Score 150.5; DB 1.1 Similarity 24.3%; Pred. No. 0.0031; 53; Conservative 23; Mismatches 5
                                                                                                                                                                                                                                                                                                   PRT; 1370 AA
LIN/NOTCH 2.
ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
MEDLINE=90017496; PubMed=2477843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95277910; PubMed=7758167;
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                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                 Query Match
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Matches 53
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anhounce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-CHAIN.
INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000494; EGRR L domain.

InterPro; IPR000494; EGRR L domain.

InterPro; IPR000494; EGRR L domain.

InterPro; IPR000401; PN_III-like.

InterPro; IPR000401; PN_III-like.

InterPro; IPR000401; Furin repeat.

InterPro; IPR000401; Forc Kinase.

InterPro; IPR000401; ReceptityTkinsII.

InterPro; IPR000401; ReceptityTkinsII.

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-1- SIMILARITY: Contains 2 fibronectin type III domains.
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InterPro; IPR000800; Notch_dom.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1 Similarity 26.7%; Pred. No. 0.0023;
47; Conservative 17; Mismatches 46; Indels 66; Gaps 11;
                                                                                                                                                                                                                                           276 ------CVDRDFCANIPNAESSDSDGFVIHDGBCAQECPSGFIRNSTQSMYC 321
                                                                                                                                                                                   232 HPB----CLGSCHTPDDNTTCVACRHYYY-------KGVCVPACPACPRGTYRFGWR-- 275
                                                                                                                                                                                                                         92 DINKCTKCKADCDTCFNKNPCTKC-----KSGPYLHLGKCLDNCPEGLEANN-HTMEC 143
                                                                                                                                                                     91
                                                                                                                                                                   35 HPNVSQGCQGGCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYY---GTRYP
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                                                                                                                                                                                                                                                                                                             322 IP---CE------GPCP---KVCG---DEEKKTKTIDSVTSAQMLQGCTILKGNL 361
757 757 N-LINKED (GLCNAC. ..) (POTENTIAL).
765 765 N-LINKED (GLCNAC. ..) (POTENTIAL).
901 901 N-LINKED (GLCNAC. ..) (POTENTIAL).
914 914 N-LINKED (GLCNAC. ..) (POTENTIAL).
1166 1166 PHOSEHORYLATION (ADTO-) (BY SIMILARITY)
985 986 AD -> PY (IN REP. 3).
1370 AA; 155395 MW; A5946897A41CB145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch protein homolog precursor (XOTCH protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=90385285; PubMed=2402639;
MEDLINE=90385285; PubMed=2402639;
"Xotch, the Xenopus homolog of Drosophila notch.";
"Soience 249:1438=1441(1990).
[2]
REVISIONS TO 1759-1782.
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InterPro; IPR001512; Asx hydroxyl_S.
InterPro; IPR000142; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001488; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
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HSSP; P00740; 1EDM.
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       TALLINGS.

-1. DENELOPMENTAL STAGE: Expressed in the brain during B14 and B17.

-1. DENELOPMENTAL STAGE: Expressed in the brain during B14 and B17.

-1. PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgin network before it reaches the plasma embrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(RC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentil in dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

-1. FTM: Phosphorylated (By similarity).

-1. SIMILARITY: Contains 3 bgf-like domains.

-1. SIMILARITY: Contains 2 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                      bonds (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (TNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.
  development, probably in some aspect of cell specification and/or differentiation (By similarity). SUBDNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor, Transcription, regulation, Activator; Differentiation, Developmental protein, Repeat, ANK repeat, EGF-like domain; Transmembrane, Glycoprotein; Signal; Phosphorylation.

SIGNAL
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SWART; SMO0179; EGF_CA; 24.
SWART; SMO0004; NL; 2.
FROSITE; PS50297; ANK_REPEAT; 4.
PROSITE; PS50089; ANK_REPEAT; 4.
PROSITE; PS00010; ASK_HYDROXYL; 22.
PROSITE; PS01186; EGF_2; 26.
PROSITE; PS01186; EGF_2; 35.
PROSITE; PS01187; EGF_CA; 22.
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InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00181; EGF_Z.
InterPro; IPR00181; EGF_Z.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR008209; Notch_Gom.
Pfam; PP00020; ank; 6.
Pfam; PP00020; ank; 6.
Pfam; PP00020; ank; 6.
Pfam; PP00020; EGF; 35.
Pfam; PP00006; notch; 2.
Pfam; PP00006; notch; 2.
PRINFS; PR00010; EGFELOOD.
PRINFS; PR00010; EGFELOOD.
PRINFS; PR00010; EGFELOOD.
PRINFS; PR00010; EGFELOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M93661; AAK13558.1; -.
PIR; A49128; A49128.
HSSP; P00743; ICCF.
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SIGNAL 1
CHAIN 26
                                                                                                                                                                                                                                                                                kidney.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           Thacker C., Srayko M., Rose A.M.;
"Mutational analysis of bli-4/kpc-4 reveals critical residues required for proprotein convertase function in C. elegans.";
Gene 252:15-25(2000).
-!- FUNCTION: The Kex2/subtilisin-like proteinase activity of this enzyme is required for the normal production of adult cuticle.
There is functional redundancy between the isoforms. Vital for embryonic and larval development.
-!- ALTERNATIVE PRODUCTS:
Event_Alternative_splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                EMBL; L29438; AAA98750.1; ALT_FRAME.

R EMBL; L29439; AAA98751.1; ALT_FRAME.

R EMBL; L2943919; AAA98752.1; ALT_FRAME.

R EMBL; AP039719; AAB96752.1; ALT_FRAME.

R EMBL; AF039719; AAB96755.1; ---

R EMBL; AF039719; AAB96755.1; ---

R MEL; AF039719; AAB96755.1; ---

R MEL; AF039719; AAB96755.1; ---

R MEL; AF039719; AAB96757.1; ALT_SEQ.

R MOXIMPEP; KO4F10.4a; CE11728.

R WOXIMPEP; KO4F10.4d; CE11730.

R WOXIMPEP; KO4F10.4d; CE11730.

R WOXIMPEP; KO4F10.4d; CE11730.

R WOXIMPEP; KO4F10.4d; CE11730.

R WOXIMPEP; RO4F10.4d; CE11730.

R GO; GO:0010612; C::Integral to membrane; NAS.

GO; GO:0004252; P::Integral to membrane; NAS.

GO; GO:0007522; P::Cuticle biosynthesis (sensu Invertebrata); IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00137; SUBTILASE SER; 1.
HYDROJARE; PS00138; SUBTILASE SER; 1.
HYDROJARE; Serine protease; Glycoprotein; Calcium-binding; Zymogen; Transmembrane; Signal; Alternative splicing.
SIGNAL.
                                                                                                                                                                        Name=A; Synonyms=a;
IsoId=P51559-2; Sequence=VSP_005416, VSP_005419;
                                                                                                                                                                                                    Name=B; Synonyms=b;
IsoId=P51559-3; Sequence=VSP_005418, VSP_005421;
                                                                                                                                                                                                                              Name=C; Synonyms=c;
IsoId=P51559-4; Sequence=VSP_005422, VSP_005423;
                                                                                                                                                                                                                                                                                                                                                                                                       shown due to erroneous gene model prediction.
                                                                                                                                             Name=D; Synonyms=d;
IsoId=P51559-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow fac recep.
InterPro; IPR002039; Peptidase S8.
InterPro; IPR002084; Peptidase S8B.
InterPro; IPR002080; Protease Inhib.
MEDLINE=20363723; PubMed=10903434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01483; P_proprotein; I.
Pfam; PF01082; Peptidase S8; I.
PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; I.
SMART; SM00261; FU; 3.
 1039
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                                                                                                                                                                                                                                                                                                                                                                                                         91 P-DINKCTKCKADCDTCFNKNFC-------TES
                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 CLD------NCPEGLEANNHTMECVSIVH-CEVSEMNPWSPCTKKGKTCGFKRGTETRV 177
                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                      985 ENNIDECTE----SSCFNGGTCVDGINSFSCLCPVGFTGPFCLHDINECSSNPCLNSGT
                                                                                                                                                                                                                                                                                                                                                      31 QRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                            89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLI4_CAEEL STANDARD; PRT; 943 AA.
P51559; 044762; 044764; 044765; 044766;
10-OCT-1996 (Rel. 34, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Endoprotease bli-4 precursor (EC 3.4.21.-) (Blistered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1040 CVDGLGTYRCTCPLGYTGKN----COTLVNLC----SP-SPCKNKG-TCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thacker C., Peters K.W., Srayko M., Rose A.M.;
"The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/aubtilisin-like endoproteases essential for early development and adult morphology.";
Genes Dev. 9:956-971 [1995].
                                                                                                                                                                                                                                                                                                DB 1; Length 2471;
                                                                                                                                                                                                                                                                                      Score 147.5; DB 1; Leury-
Pred. No. 0.005;
Pred. Tarbeles 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND FUNCTION STRAIN=Bristol N2; MEDLINE=95293228; PubMed=7774813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Latreille P., Wamsley P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1080 ----QEKARPRCLCPPGWDGAYCDVLNVSCKAAALQKG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 REIIQHPSAKGNLCPPTNETRKCTVQRKKC----QKG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A., AND ALTERNATIVE SPLICING
                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                            23; Mismatches
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                                                                                                                                                                                                                                SIMILARITY
 9.7%;
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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                             Best_Local Similarity 24.8%
Matches 54; Conservative
509
518
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547
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BY SIMILARITY. ENDOPROTEASE BLI-4. CHARGE RELAY SYSTEM (BY SIMILARITY). CHARGE RELAY SYSTEM (BY SIMILARITY). CHARGE RELAY SYSTEM (BY SIMILARITY). POTENTIAL. CYTOPIASMIC (POTENTIAL). CYS-RICH. N-LINKED (GLCNAC) (POTENTIAL).	VERSARSSFPDLT -> ILITIALHLVVNA (in lacform A). /PITGAYER 005416. VERSARSSFPDLTSGWKLSCDECNGGCTESSSATSCFAYKH L -> LCFNFRNSOPTECVCLRVCEPGVIINFQIEKLKKST KCLIPS (in isoform B). /PITGA-VSP 005417.	VEESARSSPPDLTSGWRLSCDECNGGCTESSSATSCPAYKH LIQTLARNGGSGFKCVQKCDDTYYLDGDKCKM -> GDEVV ERIRNHWEVTLEESSHWNWEHAREHKSLQELNSSSRTHSFL YSFTKFQPIFLILLVCIFDAJHRQFAV (in isoform B) /PTId=VSP_005418.	Missing (in isoform A). /FIId=VSP 005419. Missing (in isoform B). /FIId=VSP 005420.	Missing (in isoform B). //FIGH-VSP 005421. ESNLVQAKCIMRUDLGGDGYXINAVGKCDLCDSSCETCTAP GENSCEKC -> AENFOFCAKNNESGROTTVFVKFKKFSAF KDYCLKLVDLDFFFFSLLIF (in isoform C). //FIIdaVSP 005422.	43 Missing (In isoform C). /FTIG+VSP 005423. 53 A - R (IN REF. 2). 46 S -> R (IN REF. 2). 103146 MW; 401E009E6C46AD7E CRC64;	9.6%; Score 145; DB 1; Length 943; 25.6%; Pred. No. 0.0031; ive 21; Mismatches 77; Indels 50; Gaps 11;	RRMHPNVSQGCQGGCATCSDYNGCLSCKPRLPFALERIGMKQIGVCLSSCPSG 84	YVGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGIR 135	ANNHTWECVSIVHCEVSEWNEWSPCTKKGKTGFKRGTETRVREIIGHESAKGNLCPPTN 195 	KCQKG 210 KCSKG 831
116 943 202 202 4415 6684 195	. 669	730	943	943 828	943 153 346 1031	2 vati	GWKLS(NKCTK(SIVHC:	- VQRKU : : PMSCEI
21 117 202 241 415 417 413 413 195	658 658	658	700	731	829 153 346 943 AA;	Similarity 25.31; Conservative	RRMHPNVSQG ::: RSSPPDLTSGWKLSC	YYGTRYPDII 		196 ETRKCTVQRKKCQKG
PROPEP CHAIN ACT SITE ACT SITE ACT SITE TRANSMEM DOMAIN CARBOHYD	VARSPLIC	VARSPLIC	VARSPLIC	VARSPLIC VARSPLIC	VARSPLIC CONFLICT CONFLICT SEQUENCE	Query Match Best Local Sir Matches 51;	32	95	136	196
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Search completed: June 29, 2004, 17:00:16 Job time : 12.2828 secs

035171 mus musculu QBCfz2 mus musculu QBCg30 mus musculu QBEpg3 cryptospori Q9Eep4 homo sapien Q18003 caenorhabdi Q9U018 giardia lam Q42114 brachydanio O76822 branchiosto

mus musculu

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042113 brachydanio 076510 cryptospori 076510 cryptospori 086x4 homo sapien 099w4 rattus spien 099w4 rattus spien 090014 mus musculu 09470 gallus gall 092496 rattus norv 094862 homo sapien 094862 homo sapien 023832 cryptospori 091832 cryptospori 09183 cryptospori 09183 cryptospori 09183 cryptospori 09183 cryptospori 09183 cryptospori 09183 cryptospori 09189 bos taurus 099189 mus musculu 088298 mus musculu

299q41 giardia lam

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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3 HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
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SEQUENCE FROM N.A.
MAO Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.
Tang R., Chen X., Wu C.;
Submitted (MAR-2000) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 272;
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TISSUB=Placenta;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF2551057; AAK34947.1; -.
EMBL; BC022367; AAH22367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC: 20866; THSD2.
InterPro; IPR006312; Purin repeat.
InterPro; IPR009030; Grow_Fac_recep.
InterPro; IPR000894; TSP1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00269; TSP1, 1.
PROSITE; PS0092; TSP1; 1.
PROSITE; PS0092; TSP1; 1.
SRQUENCE 272 AA; 30928 MW; CACABC6B7E781189 CRC64;
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Last annotation update)
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Q96EP4
O18003
Q9U018
O42114
O76822
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Q9QW44
Q9GQ45
Q80T14
Q9W770
Q924Y6
Q9HCB6
Q9HCB6
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09B105
09GLX9
099KR2
08K2Q8
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Q9PVZ4
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Homo sapiens (Human)
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                      Best Local Sir
Matches 271;
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Q9BXY4
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Q8by2 mus musculu
Q81313 mus musculu
Q8n715 homo sapien
Q8n715 homo sapien
Q8n5x6 homo sapien
Q9n6x6 homo sapien
Q9n6x6 homo sapien
Q9n6x8 musculu
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Q8n5x3 mus musculu
Q84y18 rana escule
Q964Q2 entramoeba h
Q8szsz drosophia
Q9sz41 entamoeba h
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                                                                                                                                                                                                                                                                            1 MCHLRLISWLPIILNPWBYI.....QQKKRKVQDKQKSVSVSTVH 273
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPSAKGNI,CPPTNETRKCTVQRKKCQKGERGKKGRERKRKFDNKGESKRAIPDSKSLESS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 PFALERIGMEQIGVCLSSCPSGYYGTRYPDINECTECEADCDTCFNENPCTRCKSGFYLH 121
                                                                                    LGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGFETRVREIIQ 182
                                                                                                122 LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 181
                                                                                                                                 HPSAKGNLCPPTNETTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKBAIPDSKSLBSS 242
                                    PPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTRCKADCDTCFNKNFCFKCKSGFYLH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
HPSAKGNI/CPPTNETTR/CTVQRKKCQKGBRGKKGRBRKRKKPNKGESKBAIPDSKSLBSS
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                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Pujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai P., Hara R., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AK027346; BAB55051.1;
                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 292 Aa; 33243 MW; 01E2774AC3D4A6F8 CRC64;
                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                             KEIPEGRENKQQQKKKKVQDKQKSVSVSTVH 272
                                                                                                                                                                                 243 KEIPEGRENKQQQKKRKVQDKQKSVSVSTVH 273
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InterPro; IPR009030; Grow fac_recep.
InterPro; IPR000884; TSP1.
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00090; tsp_1; 1.
SMART; SM00261; FU; 2.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                   PRELIMINARY;
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C STRAING-CS 7BL/651, TISSUE-Embryo;

KRAING-CS 7BL/651, TISSUE-Embryo;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa M., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kahl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Bareh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Pletcher C., Fullia M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Salaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wanshaw-Borie A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Mayashizaki Y..
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
2810459404Rik protein (Fragment).
THSD2 OR 2810459404RIK.
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InterPro; IPR006212; Purin repeat.
InterPro; IPR006303; Grow_fac_recep.
InterPro; IPR00084; TSP1.
Pfam; PF00090; tsp_1; 1.
SMART; SM0021; F07; 2.
SWART; SW00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
242 KEIPEGRENKQQKKRKVQDKQKS
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Best Local Similarity 93.18
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Best Local Similarity
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Q8N7LS;
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/643; N.A.
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
The RANTOM Consortium,
The RANTOM Consortium,
The RANTOM Consortium,
Than 194516 of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMB1, AK076308; BAC36296.1; -.
MGD, WGI:1920030; Th8d2.
InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow_fac_recep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 HERLISCFFIILNFMBYIGSONASRGRRORRMHPHVSQGCQGGCATCSDYNGCLSCKPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kamata T., Katsube K., Michikawa M., Yamada M., Mizusawa H.;
"R-spondin, a novel thrombospondin type I domain gene, expressed in the dorsal neural tube.";
Submitted (MIG-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016/68; BAA75640.1; -...
MGD; MGI:2183426; Rspondin.
                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.2%; Score 1064; DB 11; Length 224; Best Local Similarity 84.6%; Pred. No. 1e-89; Matches 187; Conservative 9; Mismatches 25; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00261; FU; 2. _ _ SQUENCE 224 AA; 25398 WW; BC13B083497CFBB3 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thrombospondin type 1 domain.
RSPONDIN OR R-SPONDIN.
                                                                                   Last sequence update)
Last annotation update)
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                                              224 AA
                                                                       Created)
                                              PRT;
                                                                      23,
23,
25,
                                              PRELIMINARY;
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                                                                                 01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                      (TrEMBLrel.
                                                                                                                       THSD2 OR 2810459H04RIK.
                                                                                                         Thrombospondin homolog
                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                       NCBI_TaxID=10090;
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                   RESULT 4
QBBVW2
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EMBL, AKO9225; BACO5261; In:

InterPro; IPR00084; TSP1.

InterPro; IPR000825; TSP1.

InterPro; IPR00209; TSP1; I.

SWART; SM00209; TSP1; I.

Hypothetical proctein.

W Hypothetical proctein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 SAKGNICPPTNETRKCTVORKKKOKGERGKKG----RERKRKKPNKGESKRAIPDSKSLE 240
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         24;
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48.1%; Pred. No. 1.5e-49;
ive 36; Mismatches 69; Indels 15.
                                                                                                                                                                                                                                                                         Length 265;
InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow Eac_recep.
InterPro; IPR000804; TSP1.
Ffan; Pr00009; tsp. 1; 1.
SMART; SM00261; FU; 2.
SMART; SM00209; TSP1; 1.
PR051TE; PS0092; TSP1; 1.
SROUENCE 265 AA; 29331 MW; FFEB8964743F5963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                      42.5%; Score 644; DB 11;
46.5%; Pred. No. 4.1e-51;
ive 36; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein FLJ40906.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SSKRIPBORENKOOOK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 -----RRHKGÓÓO 247
                                                                                                                                                                                                                                                                                                                                         Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 48.1
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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OBN6X6
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  29UGB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 MAKCIKCKIEHCEACPSHAPCTKCKGGLYLHKGRCYPACPEGSSAANGTMECSSPAQCEV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNPCTKCKSGFYLHLG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTBTRVREIIQHP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAKGNLCPPTNETRKCTVQRKKKCQKGERGKKRKRKKPNKGESKRAIPDSKSLESSKR 244
                                                                                                                                                                        152 SEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRKKKCQKGE 211
                                                                                                                                                                                                 93 INKCTKCKAD-CDICFNKNPCTKCKSGPYLALGKCLDNCPEGLBANNHTMECVSIVHCEV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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6 LISWLPIILNPMEYIGSQNASRGRRQRRMHPNVSQCCQGCCATCSDYNGCLSCKPRLFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                             212 RGKKGRERKRKKPNKG----ESKEAIPDSKSLESSKEIPEQRENKQQQKKR 258
                                                                                                                                                                                                                                                                                      Match 38.0%; Score 576.5; DB 11; Length 243; Local Similarity 45.0%; Pred. No. 5.9e-45; Los 108; Conservative 39; Mismatches 78; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  243 AA
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01-MAR-2003 (TrEMBLrel. 23, Last sequence
10-CT-2003 (TrEMBLrel. 25, Last annotatio
Hypothetical thrombospondin type I repeat.
2610028F08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          QBBFU0;
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088FU0
10 088FU0
11 01-M
DT 0
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RESULT 8

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89 RYPDINKCTKCKADCDTCPNKNPCTKCKSGPYLHLGKCLDNCPEGLEANNHTMECVSIVH 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 RRORRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TremBlrel. 25, Last annotation update)
038424716.3 (Movel protein 8-spondin) (Fragment).
03824816.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 224;
                                                                                                                                                                                                                                                                                                       Blakey S.; Caber S. Blakey S.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
REMBL, ALOS0325; Caber783.3; - Genew; HGNC:16175; C20orf182.
InterPro; IPR006212; Purin repeat.
InterPro; IPR009030; Grow_Fac_recep.
InterPro; IPR009030; Grow_Fac_recep.
R SMART; SM00209; TSP1; 1.
R SMART; SM00209; TSP1; 1.
R PROSITE; PS500229; TSP1; 1.
INON_TER
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31.1%; Score 472; DB 4; Length 22
Best Local Similarity 43.3%; Pred. No. 2.1e-35;
Matches 87; Conservative 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027938; AAH27938.1; ..
InterPro; IPR065212; Purin repeat.
InterPro; IPR09030; Grow Fac_recep.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 224 AA; 25042 MW; 97D26AD34CDBFB12 CRC64;
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Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00261; FU; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to putative.
                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-Lung;
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                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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63 LRREGMRQYGECLHSCPSGYYGHRAPDMNRCARCRIENCDSCPSKDPCTKCKVGFYLHRG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 RRKKQAGTGLGGNCT-GCVICSBBNGCSTCQQRLFLFIRREGIRQYGKCVHDCPLGFFGI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 RRORRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGWKQIGVCLSSCPSGYYGT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK020904; BAC25643.1;
MGD; MGI:1924467; A930029K19Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Cieplik M., Klenk H.;
Cieplik M., Klenk H.;
"Cloning and functional characterization of FURIN from Spodoptera "Cloning and functional characterization of FURIN from Spodoptera Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
-1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.7%; Score 283.5; DB 11; Length 138; Best Local Similarity 42.9%; Pred. No. 2.5e-18; Matches 45; Conservative 24; Mismatches 35; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 RYPDINKCTKCKADCDTCFNKNPCTKCKSGPYLHLGKCLDNCPEG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00261; FU; 2. SRQUENCE 138 AA; 15172 MW; FEFD7D949279D5DD CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                 125 KCLDNCPEGLEANNHIMECUSIVHCEVSEWN 155
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InterPro; IPR009030; Grow_fac_recep.
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                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/61; TISSUB=Retina;
MEDLINB=22354683; PubMed=12466851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z68888; CAA93116.1; -.
                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                      (Mouse)
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Mus musculus (
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Q26489;
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                                                                                                                                                                       RESULT 11
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MEDLINE-2518L/63; TISSUE-Egg;

MEDLINE-2518L/63; TISSUE-Egg;

MEDLINE-2518L/63; TISSUE-Egg;

Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Nilalon D.K., Muzny D.M., Soderger B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Razywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                   ñ
                                                                                                                                           71 MKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCPNKNPCTKCKSGPYLHLGKCLDN 129
                                                                                                                                                                                                                                          130 CPEGLEANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGN 189
                                                                                                                                                                                                                                                                                     61 CPDGPAPLEETWECVE -- GCEVGHWSEWGTCSRNNRTCGPKWGLETRTRQIVKKPVKDTI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCPNKNFCTKCKSGFYLHLG 124
                                                                                                                                                                    5 LFSFALIILNCMDYSQCQ-GNRWRRNKRA-SYVSNPICKGCLSCSKDNGCSRCQQKLPFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LISWLFIILNFMEYIGSONASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFA 65
                                                                                              13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                       190 LCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLESSKE 244
                                                                                                                                                                                                                                                                                                                                                                  119 PCPTIABSRRCKMTMRHCPGGKRTPKAKEKRNKKKKR------KLIERAQE 163
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                 Length 176;
                                          Query Match
30.3%; Score 459.5; DB 4; Length
Best Local Similarity 45.1%; Pred. No. 2.3e-34;
Matches 79; Conservative 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
  20409 MW; 0F83CCE1B2F8CA85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC052844; AAH52844.1; -. SEQUENCE 152 AA; 17658 MW; B74713789B2853B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2610028F08Rik protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
  176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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  SEQUENCE
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Best Loc Matches

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Q7TPX3

9 RESULT Q7TPX3

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632 GPCDARCSDV-GCDGPGPHHCNDCLHFYYK--AKNNTRICVSDCPLGYYPA---DKKKCK 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 KCKADCDTCP--NKNPCTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSIVHCEVSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 GGC-ATCSDYNGC----LSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 WNPWSPCTKKGKTCGPKRGTETRVREIIQHP-SAKGNLCPPTNET-RKCTVQRKKCQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=HM:1MSS;
MEDLINE=21391855; PubMed=11500468;
MEDLINE=21391855; PubMed=11500468;
Cheng X.J., Hughes M.A., Rhuston C.D., Loftus B., Gilchrist C.A.,
Lockhart L.A., Ghosh S., Miller-Sims V., Mann B.J., Petri W.A. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachibana H.;

"Intermediate Subunit of the Gal/GalNAc Lectin of Entamoeba
histolytica Is a Member of a Gene Family Containing Multiple CXXC
Sequence Motifs.":

Infect. Immun. 69:5892-5898 (2001).

EMBL; AR337950; AAK92361.1;

GO; GO:0007157; P:heterophilic cell adhesion; IEA.

InterPro; IPR006209; EGP_like.

InterPro; IPR009030; Grow_fac_recep.

PROSITE; PS01186; EGP_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 179.5; DB 13; Length 913; 29.4%; Pred. No. 5.9e-08; tive 22; Mismatches 66; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.7%; Score 177; DB 5; Length 1101;
Best Local Similarity 26.6%; Pred. No. 1.2e-07;
Matches 55; Conservative 22; Mismatches 80; Indele 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1101 AA; 119512 MW; C8B6F5CBDE656AEC CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Gal/GalNAc lectin Igl1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1101 AA
                                                 InterPro; IRROGGIO; IEGF.
InterPro; IPROGGIO; IEGF.
InterPro; IPROGGIO; Peptidase_S8.
InterPro; IPROGGIO; Peptidase_S8.
InterPro; IPROGGIO; Peptidase_S8.
InterPro; IPROGGIO; Protease Inhib.
Pfam; PROGGIO; Peridase_S8; 1.
Pfam; PROGGIO; Peridase_S8; 1.
Pfam; PROGGIO; Peridase_S8; 1.
Prodem; PROGGIO; Peridase_S8; 1.
PROGITS; PROGGIO; Proprotein; 1.
SWART; SWOO181; EGF; 4.
SWART; SWOO181; EGF; 4.
SWART; SWOO181; EGF; 4.
SWART; SWOO181; EGF; 4.
PROSITE; PSGO136; SUBTILASE_ASP; 1.
PROSITE; PSGO137; SUBTILASE_ASP; 1.
PROSITE; PSGO138; SUBTILASE_SER; 1.
Furin repeat.
Grow_fac_recep.
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Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759,
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Best Local Similarity 29.4%
Matches 52; Conservative
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                             nterPro; IPR009030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 WNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNICPP---TWETRKC-TVQRKKCQK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 CTKCKADCDTCP--NKNPCTKCKSGPYLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900 ---CSTCT-----SAPCLSCEPKWELNKKGKCMPVGSDKCSA 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 NVSQGCQGCCATCSD-YNGCLSCKPRLPFALERIGMKQIGVCLSSCPSGYYGTRYPDINK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Comp. Neurol. 0:0-0(2002).

BrHL, AV131222, AAN10146-1; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0006313; F:peptidase activity; IEA.

GO; GO:0004114; F:transmembrane receptor protein tyrosine kin. .; IEA.

GO; GO:0004118; P:electron transport; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0006488; P:protein amino acid phosphorylation; IEA.

GO; GO:0006508; P:protein amino acid phosphorylation; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

GO; GO:0001169; P:transmembrane receptor protein tyrosine kin. .; IEA.

InterPro; IPR000345; CytC heme BS.

InterPro; IPR006211; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Gangmon F., Jegou S., Vallarino M., Vieau D., Vaudry H.;
Molecular characterization of the CDNA and localization of the mENA
encoding the probormone convertage PC5-A in the European green frog.";
J. Comp. Neurol. 0:0-0(2002).
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Serine procease PC5-A.
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana (NCBI_TaxID=8401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        934 GBFAV---DQKCKRCNPACDSCYGENEGHCLITCPNPNLLQDYKCVPE 977
                                                 R GO; GO:000823; F:Peptidase activity; IEA.

R GO; GO:000823; F:Peptidase activity; IEA.

R GO; GO:0004289; F:Subtilase activity; IEA.

R InterPro; IPR00512; Furin repeat.

InterPro; IPR00512; Furin repeat.

InterPro; IPR00512; Peptidase_88.

InterPro; IPR00584; Peptidase_88.

InterPro; IPR00584; Peptidase_88.

R InterPro; IPR009020; Protease Inhib.

R Pfam; PR001082; Peptidase_88; I.

R Pfam; PR01483; P. Proprofein; I.

R PRINTS; PR00723; SUBTILISIN.

R PROMOTIS; PS00114; P. domain; I.

R PROSITE; PS00137; SUBTILIASE_ASP; I.

R PROSITE; PS00137; SUBTILIASE_HIS; I.

R PROSITE; PS00138; SUBTILIASE_HIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 192; DB 5; Length 1299; 27.8%; Pred. No. 6e-09; vative 26; Mismatches 78; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last seq
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Matches 63; Conservative
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Search completed: June 29, 2004, 17:02:12
Job time : 37.7876 secs
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833 YAWQNKCLISCPDGFYADKKRLBCM-
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                            90 YPDINKCTKCKADCDTCFNKNPCTK------CKSGFYLHLGKCLDNCPRGLEA 136
                                                                                                                                                                                                                                                   885 THHCSECSSAARCTVCESDTYKVISGNGCNSCVDGF-----YPDBIKGTCIPC 932
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                                                                                                                                                                                                                 137 NNHTMECVSIVHCEVSEMNPWSPCTKKG-KTC--GFKRGTETRVREIIQHPSAKGNLCPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
GGCATCSD---YNGCL---SC----KPRLPPALB----RIGMKQIGVCLSSCPSGYYGTR 89
                                                                                                                                          3 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
Stapleton M., Broktein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friee E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LD30182p.
FURZ OR CG4235 OR CG18734.
Drosophila melanogaeter (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted Signature Signat
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1376 AA; 149716 MW; B6704BAB9A3A88FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1376 AA.
                                                                                                                                                                                                                                                                                                                         194 TNETRKCTVQRKKCOKGERGKKGRERK 220
                                                                                                                                                                                                                                                                                                                                                                            TSPCTKCVGVKKDCREQRTGCNSRKKK 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Conservative
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Best Local S
Matches 60
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120 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTXXGKTCGFKRGTETRV-R 178
                                                                                                               ---PCORGCKTC----TSNGVCS 873
784 LVMHEHK------CYSACPLDTYET---EDNKCAFCHSTCATCNGPTDQDCITCRSSR 832
                                                                                                                                                                        211
                                                                                                                                                                                                            179 BIIQHPSAKGNLCPPTNBTRKCTVQRKK-CQKGE
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Mus musculus
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1562.545 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                    Aae13167
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                            1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                OM protein - protein search, using sw model
                                                                                                                                                                                                                       Listing first 45 summaries
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AAW85607
AAB13170
ABP61846
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AAB99220
AAM78328
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AAE13150
ABR62112
ABO44432
ABO44413
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AB044427
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AB044417
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ABO44434
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ABB11374
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                                                June 29, 2004, 16:54:09
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geneseqp2002s:*
geneseqp2003as:*
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Maximum DB seq length: 200000000
                                                                                  US-09-894-912A-32
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Match Length DB
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                                                                                                   Sequence:
                                                                                                                                           Searched:
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                                                Run on:
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No.
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Aam79312 Human pro	Aael3149 Human ste	Abo44415 Human ste	Abr62108 Secreted	Abr62115 Secreted	Abr58489 Human sec	Ade07919 Novel pro	Abr62110 Secreted	Abr62113 Mouse thr	Aael3162 Mouse thr	Abo44426 Mouse thr	Aae37115 Human sec	Abg76508 DNA encod	Abr62106 Secreted	Aae36166 Mouse SCR	Abr62101 Secreted	Abr62107 Secreted	Abr62102 Secreted	Adb76146 Novel hum	Aael3155 Human SCR
AAM79312	AAE13149	ABO44415	ABR62108	ABR62115	ABR58489	ADE07919	ABR62110	ABR62113	AAE13162	AB044426	AAB37115	ABG76508	ABR62106	AAE36166	ABR62101	ABR62107	ABR62102	ADB76146	AAB13155
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160	160	160	263	263	263	263	243	265	229	229	243	243	243	243	250	222	229	234	46
49.4	49.4	49.4	42.2	42.2	42.2	42.2	41.7	41.2	41.0	41.0	37.2	37.1	37.1	36.8	36.8	34.9	34.6	29.3	17.4
759	759	759	648	648	648	648	640.5	632	629	629	571.5	569.5	569.5	565.5	565	536	531.5	450	267
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Mouse; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; dancher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder, autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                   Mouse stem cell growth factor-like protein.
AAE13167 standard; protein; 279 AA
                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                         28-JAN-2002
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22. .279
/note= "Mouse mature stem cell growth factor-like
protein" 1. .21 /label= Signal_peptide Location/Qualifiers #0200177169-A2 18-0CT-2001

05-APR-2001; 2001WO-US011208

05-APR-2000; 2000US-00543774. 28-UUV-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757562. 05-PRB-2001; 2001US-0266614P.

(HYSE-) HYSEQ INC. (KIRI) KIRIN BEER KK.

Drmanac RT; ပဲ Liu Tang TY, Labat I, Tillinghast JS, Sinku A,

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The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell, plantipotent cell, hasmatopoietic progenitor cell, pluripotent cell, hasmatopoietic progenitor cell, pluripotent cell, hasmatopoietic progenitor cell, pluripotent cell or totipotent cell. The hasmatopoietic progenitor cell, pluripotent cell or totipotent cell. The hasmatopoietic progenitor cell, pluripotent cell or totipotent cell. The hasmatopoietic progenitor cell, pluripotent cell or totipotent cell. The hasmatopoietic progenitor cell cultured using stem cell growth factor-like proteins can replace as agraft for the bone marrow cramplantation or cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, hasmana, hasmana, acquired immune deficiency syndrome (AIDS), thalassaemia, hasmalytic anaemia due to enzyme defect, congenital anaemia cult as sickle cell anaemia daucher such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases uch as parkinson's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiency concernia, immune deficiencies and diseorders such as severe combined immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from mouse
                                                                                                                                                    Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's
                                                                                                                                                                                                                     disease, cancer, rheumatoid arthritis, osteoporosis
Nishikawa M;
                                                                                                                                                                                                                                                                               Claim 28; Page 223-224; 232pp; English.
Mize NK,
Stache-Crain B, Dickson M,
                                                             2001-657166/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 279 AA;
                                                                                          N-PSDB; AAD21727
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61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNFCTKCKSGFYL 120 181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKTANKEERKETSSSSDSK 240 LPFVLBRIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGFYL 120 HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180 181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSK 240 9 9 1 MHIRLISCPFIIINPMEYIGSQNASRGRRQRRWHPNVSQCCQGCATCSDYNGCLSCKPR 1 MHLRLISCPFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR Gaps ö 100.0%; Score 1535; DB 4; Length 279; 100.0%; Pred. No. 6.2e-109; ive 0; Mismatches 0; Indels 0 Query Match
Best Local Similarity 100.
Matches 279; Conservative 61 121 셤 셤 Š 셤 ઠે 셤 è

GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279 ABO44431 standard; protein; 279 AB044431; RESULT 2
AB044431
ID AB04
XX
AC AB04
XX
DT 30-S
XX
DS MOUS
XX

241 GLESSIETPDQQENKERQQQKRRARDKQQKSVSVSTVH 279

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Mouse stem cell growth factor-like protein.

(first entry)

30-SEP-2003

/note= "Mature stem cell growth factor-like protein. This protein is specifically claimed in claim 9" immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; atromal cell; halbs; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; mouse. cell growth factor-like protein; antianemic; anti-HIV; SCR-1; 1. .21 /label= Signal_peptide Location/Qualifiers US2003044792-A1. Aus musculus 06-MAR-2003 Peptide Protein

28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-026614P. 05-APR-2001; 2001US-0282397P. DRMANAC R T. NISHIKAWA M. CHAO C. TANG Y T. LABAT I MIZE N. (TANG/) (LABA/) (NISH/) (DRMA/)

28-JUN-2001; 2001US-00894912

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells. WPI; 2003-625403/59. N-PSDB; ACH04327

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Mize N, Nishikawa M,

Drmanac RT,

Labat I,

Tang YT,

Claim 23; Page 80; 96pp; English.

The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding complement of the polymucleotide, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide, a m (expression) vector comprising the SCR-1 polymucleotide, a host cell genetically engineered to contain the SCR-1 polymucleotide in the host controls expression of the polymucleotide in the host cell, that controls expression of the polymucleotide in the host cell, preparation of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide having an equivity to support proliferation or survival of haematopoietic stem cell, with a proviso that C-terminal as sequence does not comprise the as sequence appearing as ABA44313), an isolated solypeptide

I lacking any 10 consecutive ass from ABA4430, an isolated polypeptide

SCR-1 polypeptide with stem cell growth factor activity and isolated polypeptide with stem cell growth factor activity having at least an as sequence appearing as ABO4428 and ABO4429, a culture medium comprising the SCR-1 polypeptide to maintain survival of or promote proliferation of a stem cell or germ cell, an anti-SCR 1 antibody, a nucleic acid array comprising the SCR-1 polymucleotide or a unique segment of the SCR-1 polymucleotide, a stromal cell genetically

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engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell genetically engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell. The SCR-1 polypeptide and for maintaining survival of or promoting proliferation of a stem cell, a germ cell, a germ cell, a germ cell, a newatopoietic stem cell or promoting proliferation of a stem cell. The SCR-1 polypeptide is useful for promoting wound healing. The human haematopoietic stem cell or a hematopoietic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation of haematopoietic stem cells can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Andrich syndrome, AIDS, etc., thalsasaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth, and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a mouse SCR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 HIGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMCKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHLRLISCPPIILNPMBYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
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malignant tumour; haemopathy; HIV infection; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1535; DB 6; Length 279; 100.0%; Pred. No. 6.2e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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IID AAB9
XX AAB9
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The present sequence is the protein sequence for human thrombospondin-30. Thrombospondin-30 protein and coding sequence are useful in the diagnosis and treatment of malignant tumour. haemopathy, HIV infection, immunological diseases and various inflammation diseases. In addition thrombospondin-30 protein may be used for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The thrombospondin-30 coding sequence may be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or in producing gene chips or microarrays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                             Human thrombospondin-30 and polynucleotide is useful in diagnosis and
treatment of, e.g., malignant tumor, hemopathy, HIV infection,
immunological diseases and various inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MHIRLISWIPTILWPWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPWSPCMKKGKTCGPKRGTETRVRDIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 1315.5; DB 4
87.1%; Pred. No. 3.1e-92;
tive 11; Mismatches 18;
                   (BIOR-) BIOROAD GENE DEV LTD SHANGHAI
                                                                                                                                                                                                                     Claim 1; Page 27-28; 33pp; Chinese.
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                                                                                         WPI; 2001-397948/42.
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                                                                                                          N-PSDB; AAH45131
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 272 AA;
                                                     Xie Y;
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemantopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                             Xu C, Cao Y;
, Chen R, Wang ZW;
                                                                                                                                                                                                                               Drmanac RT, Asundi V, Zhou P, X
Pang D, Wang J, Zhang J, Ren P,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 3214-3215; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        diagnosis and gene therapy.
                                                                      19-JUL-2000; 2000US-00620325.
01-SBP-2000; 2000US-00654936
115-SBP-2000; 2000US-0065351.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                                                                                 Wang D, Wang
Wejhrman T,
                  03-FBB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
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N-PSDB; AAK51461.
                                                                                                                                                                                                           Tang YT, Lie,
Ma Y, Zhao QA, We,
                                                                                                                                                                                           (HYSE-) HYSEQ INC
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Sequence 272 AA;

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LPPVLARICMKOIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGPYL 120
                                                                                                                                    61 LPPALERIGMEGIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGPYL 120
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                                                                                                                                                                                               QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEERKBTSSSSDSK 240
                                                                                                                                                                                                                                                         MHLRLISCFFIILNFMBY1GSONASRGRRORRMHPNVSQGCQGCATCSDYNGCLSCKPR
                             Gaps
                          7;
DB 4; Length 272;
                             18; Indels
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85.7%; Score 1315.5; DB 87.1%; Pred. No. 3.1e-92;
                             11; Mismatches
                             Matches 243; Conservative
              Local Similarity
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   Query Match
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AAB13168 standard; protein; 272 AA

28-JAN-2002 (first entry)

AAE13168;

RESULT 5
AAE13168
ID AAE1
XX
AC AAE1
XX
DT 28-J

Human stem cell growth factor-like protein #4

Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliaer; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; dancher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.

Homo sapiens.

22. .272 /note= "Human mature stem cell growth factor-like protein" 1. .21 /label=_Signal_peptide Location/Qualifiers Peptide Protein

WO200177169-A2.

18-0CT-2001.

05-APR-2001; 2001WO-US011208.

28-JUN-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757562. 05-FBB-2001; 2001US-0266614P. 05-APR-2000; 2000US-00543774.

(HYSE-) HYSEQ INC. (KIRI) KIRIN BEER KK

Drmanac RT; Labat I, Tillinghast JS, Sinku A, Liu C, in B, Dickson M, Mize NK, Nishikawa M; Stache-Crain B, ĭ Tang

WPI; 2001-657166/75. N-PSDB; AAD21728.

Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.

Claim 28; Page 226-227; 232pp; English.

The patent discloses novel stem cell growth factor-like proteins and polynucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, perm line stem cell, embryonic stem cell, hematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell growth centralike proteins can replace as a graft for the home marrow transplantation or cord blood transplantation for treating a variety of diseases uch as immunodeficiency syndrome, chronic granulomatous disease, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immune deficiency syndrome (ALDS), thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia cuch as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Parkinson's disease, Alzheimer's are useful for treating diseases such as parkinson's disease. Alzheimer's are useful for treating diseases such as Parkinson's disease. Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary

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Human, stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquillierer; cerebroprotective; ossteopathic; immunodeficiency syndrome; chronic gramulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
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inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from human
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                                                                                                                                                                              1 MHLRLISWLFIILNPMEYIGSQNASRGRRQRRMFPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                             OHPSAKGKGNLCPPTSETRTCIVORKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSK
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                                                                                     85.7%; Score 1315.5; DB 4; Length 272; 87.1%; Pred. No. 3.1e-92; ive 11; Mismatches 18; Indels 7;
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/label= Signal_peptide
22. .272
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2001US-00757562.
2001US-0266614P.
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                                                                                   Query Match
Best Local Similarity 87.1%
Matches 243; Conservative
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                                                   Sequence 272 AA;
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28-JUN-2000; 2
09-JAN-2001; 2
05-PEB-2001; 2
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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell which is preferably primordial germ cell, garm this stem cell embryonic stem cell, promotic stem cell, propentior cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell intense cell immunodeficiency syndrome, chronic granulomatous diseases uch as immunodeficiency syndrome, chronic granulomatous (Miskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS). Thalassaemia, haemalytic anaemia due to enzyme defect, congenital anaemia cuch as sickhe cell anaemia daucher's disease, lypoisomal storage diseases such as mucopolysaccharidosis, adrenal white matter degeneration, a variety of cancer and tunnours. Proteins of the invention care useful for treating diseases such as Parkinson's disease, Alzhaimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as multiple sclerosis, systemic lupus arythematosus, rheumatoid arthritis, and autoimmune plumonary chlupus arythematosus, rheumatoid arthritis, and autoimmune plumonary chlupus arythematosus, rheumatoid arthritis, and autoimmune plumonary chlupus arythematosus, theumatoid arthritis, and autoimmune plumonary chlupus arythematosus, rheumatoid arthritis, and autoimmune plumonary chlupus arythematosus, rheumatoid arthritis, and autoimmune plumonary che are also useful in gene them tell growth factor-like protein from human
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                                                                                                                                                                                                                                                    Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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Stache-Crain B, Dickson M, Mize NK, Nishikawa M,
                                                                                                                                                                                                                                                                                                                                                                  Claim 28; Page 211-212; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
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                      HYSEQ INC.
KIRIN BEER KK.
                                                                                                                                                                                WPI; 2001-657166/75.
                                                                                                                                                                                                        N-PSDB; AAD21724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 272 AA;
                   (HYSE-) )
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AC ABR6
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06-MAR-2003
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(MIZB/)
(NISH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and polymucleotides. The stem cell growth factor-like polypeptides and polymucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerative diseases like Alzheimer's disease. They are also useful for generating new tissues and organs that may aid patients in need of transplanted tissues. The polymucleotides are useful as hybridisation probes, oligomers or primers for PCR, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERRRKKTANKEERKETSSSSDSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LPFVLERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCTVDCDTCFNKNPCTKCKSGFYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome and gene mapping, in recombinantly producing protein, in generating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically bind the polypeptide, as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the polypeptides or polynucleotides are useful for the diagnosis, treatment or prevention of cancers, and other immunological disorders. The current sequence represents a human clone 1 thrombospondin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new stem cell growth factor-like polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPWVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHLRLISCPPIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                 Human; secreted; stem cell growth factor; cytostatic; haemostatic; neuroprotective; immunostimulant; leukaemia; haemophilia; cancer; degenerative disease; Alzheimer's disease; food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Score 1115.5; DB 6; Length 272; 87.1%; Pred. No. 3.1e-92; ive 11; Mismatches 18; Indels 7;
                                  Human clone 1 thrombospondin protein #23
                                                                                                                          immunological disorder; thrombospondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pig 1; 151pp; English
                                                                                                                                                                                                                                                                                                          30-AUG-2001; 2001US-0316368P.
10-DEC-2001; 2001US-0339739P.
19-APR-2002; 2002US-00125852.
                                                                                                                                                                                                                                                                       10-AUG-2002; 2002WO-US027746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 243; Conservative
18-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-381616/36.
                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 272 AA;
                                                                                                                                                                                                   WO2003029405-A2
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                     10-APR-2003.
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22. .272 // Adding stem cell growth factor-like protein. This protein is specifically claimed in claim 9"
181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGBSKB--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant; vulnerary; hematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; hematopoietic progenitor cell; stromal cell; hlub; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; hemolyfic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or ragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polynucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΰ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell growth factor-like protein; antianemic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mize N, Nishikawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human stem cell growth factor-like protein, SCR 1 #4.
                                                                            241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                             237 SLESSKEIPEGRENK--OOOKKKKVODK-OKSVSVSTVH 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .21
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                       ABO44432 standard; protein; 272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Page 82; 96pp; English.
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05-FBB-2001; 2001US-026614P.
05-APR-2001; 2001US-0282397P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-2003 (first entry)
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MIZE N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANG Y T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LABAT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACH04328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo gapiens
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CC SCR-1 polymucleotide, a host cell genetically engineered to comprising the SCR-1 polymucleotide, a host cell genetically engineered to comprising the SCR-1 polymucleotide in operative association with a regulatory sequence that controls expression of the polymucleotide in the host cell, the polymucleotide in the host cell, controls expression of the polymucleotide in the host cell, controls expression of the polymucleotide in the host cell, controls expression of the SCR-1 polymeleotide in the polypeptide and cativity to support proliferation or survival of haematopoietic stem cell activity and comprise the as sequence appearing as ABO44433), an sequence does not comprise the as sequence appearing as ABO44433, an isolated SCR-1 polypeptide with stem cell growth factor activity and isolated polypeptide control factor activity having at least an as sequence appearing as ABO4432 and ABO4433, a nucleic actid array cell or germ cell, an anti-SCR_1 antibody, an uncleic acid array cell or germ cell, an anti-SCR_1 antibody, an uncleic acid array comprising the SCR-1 polymeleotide or a unique segment of the SCR-1 polymeleotide or stranded to a surface, a stronal cell genetically propried to stranded to a surface, a stronal cell genetically compressed the SCR-1 polymeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell cypreptide and for maintening survival of or promoting yound control or propertide and for maintening survival of or promoting yound control or propertide and for maintening survival of or promoting yound control or propertide and for maintening survival of or promoting yound chall, a hematopoietic stem cell or promoting wound chaling. The bunn hematopoietic stem cell or human hematopoietic stem cell or the conventional bone marrow transplantation or cord blood transplantation. The transplantation of heamatopoietic stem cell or the conventional bone marrow transplantation or cord blood transplantation or treat immunofficiency syndrome, and propertide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1
complement of the polynucleotide), an (expression) vector comprising the
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85.7%; Score 1315.5; DB 6; Length 272; 87.1%; Pred. No. 3.1e-92; ive 11; Mismatches 18; Indels 7; Query Match 85.7%; Best Local Similarity 87.1%; Matches 243; Conservative Sequence 272 AA;

121 HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180 191 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLANKERKETSSSSDSK 240 181 QHPSA--KGNLCPPTWETRXCTVQRKKCQKGERGKKGRERKRKKDNKGESKE--AIPDSK 236 61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGFYL 120 121 HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180 9 9 1 MHLRLISCFFIILNFMBYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR 1 MHIRLISWIFILLNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR Gaps 7; 61 윱 ò 윱 Š 셤 è 셤

ABO44413 standard; protein; 272 AA ABO44413; AB044413 SXXX

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(first entry) 30-SEP-2003 Human stem cell growth factor-like protein, SCR 1 #1

congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; haematomy transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich syndrome; haemolytic anaemia; Stem cell growth factor-like protein; antianemic; anti-HIV;

Homo sapiens.

JS2003044792-A1

06-MAR-2003.

8-JUN-2001; 2001US-00894912.

28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P.

LABAT I. DRMANAC R T. TANG Y T. (TANG/) LABA/

MIZE N. (MIZE/) (DRMA)

NISHIKAWA M

CHAO C. (NISH/) (CHAO/) Chao C; Mize N, Nishikawa M, lang YT, Labat I, Drmanac RT,

Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells. N-PSDB; ACH04323, ACH04324. WPI; 2003-625403/59

Claim 23; Fig 3; 96pp; English.

The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polynucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polynucleotide), an (expression) vector comprising the SCR-1 polynucleotide, a host cell genetically enginered to contain the SCR-1 polynucleotide in the host cell, that controls expression of the polynucleotide in the host cell, that controls expression of the polynucleotide in the host cell, corpus the SCR-1 polymeptide, a polypeptide in the host cell, corpus or expression product of the SCR-1 polynucleotide (the polypeptide having an expression product of the SCR-1 polynucleotide (the polypeptide having an expression product of the SCR-1 polynucleotide (the polypeptide having an extrivity to support proliferation or survival of haematopoietic stem cell, such as sequence does not comprise the as sequence appearing as ABO44413), and isolated SCR-1 polypeptide with stem cell growth factor activity having at least an as sequence appearing as ABO44428 and ABO44429, a culture medium comprising the SCR-1 polypeptide or a unique segment of the SCR-1 polymentiacion of a stem cell or maintain survival of or promote proliferation of a stem cell or comprise or a surface, a stromal cell array or proport or autivity and a provise the cell or maintain survival of or promote proliferation or a surface or a unique segment of the SCR-1 polymentale. engineered to express the SCR-1 polypeptide to support proliferation c survival of a stem cell or germ cell and an implant comprising a cell genetically engineered to express the SCR-1 polypeptide to support WO200177169-A2

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proliferation or survival of a stem cell or germ cell. The SCR-1

CC polypeptide and for identifying a compound that binds to the SCR-1

CC a stem cell, a germ cell, a haematopoietic stem cell or a haematopoietic

C a stem cell. The SCR-1 polypeptide is useful for promoting wound

CC progenitor cell. The SCR-1 polypeptide is useful for promoting wound

CC progenitor cell culture using the SCR-1 polypeptide can replace as a

CC graft for the conventional bone marrow transplantation or cord blood

CC transplantation. The transplantation of haematopoietic stem cells can be

CC progenitor cell culture using the SCR-1 polypeptide can replace as a

CC graft for the conventional bone marrow transplantation or cord blood

CC transplantation. The transplantation of haematopoietic stem cells can be

CC wiskott. Aldrich syndrome, AlbS, etc., thalassaemia, haemolytic anaemia

CC disease, duplicated immunodeficiency syndrome, agammaglobulinaemia,

CC wiskott. Aldrich syndrome, AlbS, etc., thalassaemia, haemolytic anaemia

CL disease etc. the SCR-1 polypeptide is useful for cell growth and

CC disease etc. the SCR-1 polypeptide is useful for cell growth, epithelial

CC morphogenesis, including tissue specific stem cell growth, epithelial

CC ell growth and regulation, ovarian follicle development, promoting nerve

CC growth and immunosuppression. The present sequence is a Human SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
           $$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 272 AA;

61 LPPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCRADCDTCFNKNFCTKCKSGFYL 120 121 HIGKCLDNCPEGIEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREII 180 61 LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNKNPCTKCKSGFYL 120 HIGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGPKRGTETRVRDIL 180 OHPSAKGKGNI,CPPTSETRTCI VORKKCSKGERGKKGRERKRKKLINKEERKETSSSSDSK 240 181 ÓHPSA - KGNLCPPINETRKCTVÓRKKCÓKGERGKKGRERKRKKPNKGESKE--AIPDSK 236 9 9 1 HILLISWLPIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 1 MHLRLISCPFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR Gaps 7; Query Match 85.7%; Score 1315.5; DB 6; Length 272; Best Local Similarity 87.1%; Pred. No. 3.1e-92; Matches 243; Conservative 11; Mismatches 18; Indels 7; 241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279 237 SLESSKEIPEQRENK--QQQKKRXVQDK-QKSVSVSTVH 272 121 181 a 셤 ઠે 셤 ે è 셤 ઠે 셤

AAE13151 standard; protein; 273 AA AAB13151; RESULT 10 AAE13151

28-JAN-2002 (first entry

Human stem cell growth factor-like protein #3.

Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; chronic granulomatous disease; aducher's acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; aducher's disease; lysosomal storage disease; uncopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.

Homo sapiens

HPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSKG 241

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or cell growth factor-like proteins are useful for supporting proliferation or cell, germ cell, germ cell, embryonic stem cell, parmatopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cells and immunodeficiency syndrome, chronic granulomatous diseases such as immunodeficiency syndrome, chronic granulomatous (Miskot-Aldrich syndrome, acquired immune deficiency syndrome (AlbS), thalassaemia, haemalytic anaemia due to enzyme defect, congenital anaemia culture as sickle cell anaemia due to enzyme defect, congenital anaemia cells as much as millians sorting diseases unch as mater diseases, lysosomal storage chaesase and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequence is stem cell growth factor-like protein from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                                                                                                                         Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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                                                                                                                                                                                                                                                                                  Drmanac RT;
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                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                             Tillinghast JS, Sinku A, Liu (
ckson M, Mize NK, Nishikawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 28; Page 214-215; 232pp; English
                                                                                                                  05-APR-2000; 2000US-00543774.
28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-0075552.
05-FEB-2001; 2001US-0266614P.
                                                                            05-APR-2001; 2001WO-US011208
                                                                                                                                                                                                                                                                     Labat I, Titter Dickson M,
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Matches 242; Conservative
                                                                                                                                                                                                                      (HYSB-) HYSEQ INC.
(KIRI ) KIRIN BEER KK.
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-657166/75.
N-PSDB; AAD21725.
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                                          18-OCT-2001
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The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide), an (expression) vector comprising the SCR-1 polymucleotide, an operative association with a regulatory sequence or strain of the SCR-1 polymucleotide in the host cell, that controls expression of the SCR-1 polymucleotide in the host cell, caparation of the SCR-1 polymucleotide (the polypeptide having an activity to support proliferation or survival of haematopoietic stem cell or hematopoietic stem cell or hematopoietic stem cell or hematopoietic progenitor cell, with a proviso that C-terminal as sequence does not comprise the as sequence appearing as ABO44433), an
                                                                                                                                                                                                                                                                                                              immunostimulant; vulnerary; hematopoletic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; hematopoletic progenitor cell; stromal cell; halbs; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor
                                                                                                                                                                                                                                                                                                 Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pang YT, Labat I, Drmanac RT, Mize N, Nishikawa M, Chao C;
                                                                                                                                                                                                                                                          Human stem cell growth factor-like protein, SCR 1 #2.
                    242 LESSIBTPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 72-73; 96pp; English.
                                                                                                                                       ABO44414 standard; protein; 273 AA
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05-FEB-2001; 2001US-0266614P.
05-APR-2001; 2001US-0282397P.
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                                                                                                                                                                                                                     30-SBP-2003 (first entry)
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NISHIKAWA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-625403/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                              AB044414;
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(NISH/)
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isolated SCR-1 polypeptide with stem cell growth factor activity and lacking any 10 consecutive aas from ABO4430, an isolated polypeptide with stem cell jarowth factor activity having at least an as sequence appearing as ABO44428 and ABO44430, a culture medium comprising the SCR-1 polypeptide to maintain survival of or promote proliferation of a stem cell, an anti-SCR autionody, a nucleic acid array.

CC comprising the SCR-1 polymuclecide or a unique segment of the SCR-1 polymuclectide or a unique segment of the SCR-1 polymptide to support proliferation or survival of a stem cell and an implant comprising a cell control survival of a stem cell or germ cell. The SCR-1 polymptide to support the SCR-1 polymptide is useful for promoting proliferation or survival of a stem cell or germ cell. The SCR-1 polymptide is useful for promoting wound a stem cell, a germ cell, a harmatopoietic stem cell or a haematopoietic stem cell or a haematopoietic stem cell or a haematopoietic stem cell or correspondent or cord blood transplantation. The transplantation of haematopoietic stem cells can be graft for the conventional bone marrow transplantation or cord blood diseases duplicated immunodeficiency syndrome, agammaglobulinemia, due to enzyme defect, congenital anaemia such as sicklaemia, daucher's disease etc. the SCR-1 polypeptide is useful for cell growth and cepulation, ovarian follicle development, promoting nor properior cell growth, sustaining meuronal populations, cartilage remodelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 HPSAKGKGNICPPTSETRTCIVQRKKCSKGERGKKGRERKRKKKANKEERKETSSSSDSKG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85607 standard; protein; 292 AA
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Matches 24
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Homo sapiens

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vasotropic; virucide; dermatological; tranquilliser; cerebroprotective
   8
                                                                                                                                                                                                                                                                                          of clones ci254 (AAV83132), da2286 (AAV83133), du4105 (AAV83134), eh801 (AAV83135), er5691 (AAV83136), fh1235 (AAV83137), fm601 (AAV83139) or fr4732 (AAV83139), all clones are deposited as ArCC 98415) and the proteins they encode are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical activity, immune system boosting activity. The polynucleotides are also believed to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LPPALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 HLGKCLDRCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKFNKGBSKB--AIPDSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 OHPSAKGKGNLCPPTSBTRTCIVQRKKCSKGERGKKGRERKRKUNKBERKBTSSSSDSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                            New polynucleotides encoding secreted human proteins - are derived from human foetal brain, adult brain, adult blood or placenta cDNA libraries, useful, e.g. as potential immunomodulators.
                                                                                                                                                                                                                                                                                The nucleotide sequence (NS) of the full-length protein-coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHLRLISCPFILLNPMEYIGSQNASRGRRQRRMHPNVSQGCQGGGATCSDYNGCLSCKDR
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                                                                                                                                         Lavallie ER, Racie LA, Merberg D, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.2%; Score 1293; DB 2; Length 292; Best Local Similarity 85.1%; Pred. No. 1.7e-90; Matches 235; Conservative 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 SLESSKEIPEQRENK--QQQKRKVQDKQKSGIEVT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GLESSIETPDOOENKERQQQQKRRARDKQQKSVSVS 276
                                                                                                                                                                                                                                                         Claim 8; Page 63-64; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE13170 standard; protein; 292 AA.
                                                           98WO-US008336
                                                                                97US-00845296
98US-00065125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SCR-1 related protein.
                                                                                                                                          Jacobs K, Mccoy JM, Lava
Spaulding V, Agostino MJ;
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                                                                                                                  (GEMY ) GENETICS INST INC
                                                                                                                                                                           WPI; 1999-024059/02.
                                                                                                                                                                                      N-PSDB; AAV83133
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 292 AA;
                                                          24-APR-1998;
              WO9849302-A1
                                                                                 25-APR-1997;
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                                                                                             23-APR-1998;
                                    05-NOV-1998
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The patent discloses novel stem cell growth factor-like proteins and solymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, paramatopoietic stem cell, mematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic stem cell. pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth factor. Ike proteins can replace as a graff for the bone marrow cell can can replace as a graff for the bone marrow cell can can cord blood transplantation for treating a variety of disease such as immunodeficiency syndrome, choose and diseases, lysosomal storage diseases, uplainated an anemia degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders such as multiple sclerolas, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is human SCR-1 related protein
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osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; agammaglobulinaemia; thalassaemia; daucher; sissease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autocimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthitis; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
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84.2%; Score 1293; DB 4; Length 292;
Best Local Similarity 85.1%; Pred. No. 1.7e-90;
Matches 235; Conservative 14; Mismatches 21; Indels 6
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Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
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28-JJN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-PBB-2001; 2001US-0266614P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSB-) HYSBQ INC.
(KIRI ) KIRIN BEER KK.
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                                   61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                                                           121 HLGKCLDSCPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                               QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic
                                                                                                                                                                                                                                                                                                                                Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; noctropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; antiulcer; fungicide; antidiabetic; actiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
1 MHLRLISWLPIILNPWRYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted or transmembrane protein and polymucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
                      LPPVLERIGMKQ1GVCLSSCPSGYYGTRYPD1NKCTKCKVDCDTCPNKNFCTKCKSGFYL
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                                                                                                                                                            241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVS 276
                                                                                                                                                                       237 SLESSKEIPEQRENK--QQQXCRKVQDXQKSGIEVT 270
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Spaulding V;
                                                                                                                                                                                                                                           ABP61846 standard; protein; 292
                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000US-00745763.
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MCCOY J M.
LAVALLIE B R.
COLLINS-RACIE L A.
BVANS C.
                                                                                                                                                                                                                                                                                        (first entry)
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corper mammalian proteins. (I) shills, where the process is subscining, treating or ameliorating a medical condition, especially immunological treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours. (I) eshibites activity relating to angiogenesis, cytokine, cell prowth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic central and peripheral nervous system diseases and neuropathies, such as Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic activity, regulation of haematopolesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopaenia and for resemeration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or regeneration and treatment of lung or liver fibrosis, reperfusion injury or various tissues, various immune deficiencies and disorders including cerver combined immunodeficiency (SCID), bacterial or tungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, cecombinant protein, as markers for tissues in which the corresponding protein is preferentially expensed and in gene therapy. The present
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(cDNA) inserts (II), where the protein is substantially free from
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84.2%; Score 1293; DB 5;
Best Local Similarity 85.1%; Pred. No. 1.7e-90;
Matches 235; Conservative 14; Mismatches 21;
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The invention relates to new stem cell growth factor-like polypeptides and polymucleotides. The stem cell growth factor-like polypeptides and polymucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerative diseases like Alzheimer's CC disease. They are also useful for generating new tissues and organs that CC may aid patients in need of transplanted tissues. The polymclectides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in complimantly producing protein, in companionately producing protein, in companionately producing protein, in the polypeptides are useful for generating antibodies that specifically bind the polypeptides are useful for generating antibodies that specifically conditionately protein or amino acid supplement, and as a food cultrappendent (e.g. procein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current cor prevention of cancers, and other immunological disorders. The current cor prevention of cancers, and other immunological disorders. The current cor prevention of annears a human secreted protein clone da_288_6
                                                                                                                                                                                                                                                                                                                                             New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
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84.2%; Score 1293; DB 6; Length 292;
Best Local Similarity 85.1%; Pred. No. 1.7e-90;
Matches 235; Conservative 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVS 276
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                                                                                                                                        30-AUG-2001; 2001US-0316368P-
10-DEC-2001; 2001US-0339739P-
19-APR-2002; 2002US-00125852.
                                                                                                  30-AUG-2002; 2002WO-US027746
                                                                                                                                                                                                                                                                                                        WPI; 2003-381616/36.
                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 292 AA;
                   WO2003029405-A2
                                                           10-APR-2003
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rch completed: June 29, 2004, 16:59:52 time: 51.7836 sec8

Search Job tim

2, Appli 3, Appli 4, Appli 4, Appli 4, Appli 2, Appli 17, Appli 17, Appli 2, Appli 3, Appli

Sequence Sequence Sequence

-08-746-559A-2 -08-864-641B-18

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ALIGNMENTS

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US-09-188-930-332
US-09-312-283C-192
                    US-08-844-641B-18
US-09-343-551-2
US-09-343-551-2
US-09-907-794A-4
US-09-907-794A-4
US-09-905-125A-4
US-09-905-125A-4
US-09-113-825-2
US-09-113-825-2
US-09-132-769-3
US-09-132-769-3
US-09-132-769-3
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 56; Conserv
139.5
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7, Appli
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                                                     June 29, 2004, 16:57:05; Search time 14.5595 Seconds (without alignments) 989.298 Million cell updates/sec
                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Sequence 23, Sequence 21, Sequence 21, Sequence 21, Sequence 18, Sequence 18, Sequence 18,
                                                                                 US-09-894-912A-32
1535
1 MHLRLISCPFIILNPMBYIG.......QQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                                                                                                                                                                                                                                Sequence 2,
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-525-940-21
US-08-525-940-21
US-08-525-940-18
US-08-214-5558-7
US-09-214-5558-7
US-09-214-5558-7
US-08-976-838-15
US-08-976-838-15
US-07-862-0218-14
PCT-US93-03164-14
US-07-862-0218-10
US-07-862-0218-10
US-08-313-2888-10
                                                                                                                                                        Fotal number of hits satisfying chosen parameters:
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PCT-US93-03164-10
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US-09-713-550-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-857-076-103
                                                                                                                                         389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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                                                                                                                                                                                                                              Database :
                                                                                                   Sequence:
                                                                                                                                          Searched:
                                                     Run on:
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737 YPGDTAARRCRR-----CHKGCETCSSRAATQCLSCR-RGPY-----HHQEMNT 779
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Sequence 2, Application US/08284941

Patent No. 5863756

GENERAL INFORMATION

APPLICANT: RIFFER, MICHAEL C

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND TITLE OF INVENTION: COMPOSITIONS AND POLYPEPTIDES IN CELLS NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSER: COCIETY COMPUSITION CONTRACTOR COLING ADDRESSER: COCIETY COMPUSITION CONTRACTOR COLING ADDRESSER: COCIETY COMPUSITION CONTRACTOR COLING ALTO SQUARE

CITY: PALO ALTO

STREET: CALIFORNIA

COUNTRY: USA
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23.3%; Pred. No. 1.2e-07;
tive 23; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/01US
TELEFOM: (415) 843-5070
TELEFOM: (415) 843-5070
TELEFAX: 380816 COOLEY PA
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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                                                                                                                                                                                                 159 CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSBTRTCIVQRK 206
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CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NPCTKCKSGFYLHLGKCLDSCPEGLE 134
                                                                                                    --- PWSP 158
                                                                                                                                                                                                                                                 898 CRRCDENCLSCAGSSRNCSRCKTGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 YIGSONASRGRRORRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLPFVLERIGMKQIGV 75
                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08447642

Patent No. 5989890

GENERAL INFORMATION:
APPLICANT: RIERR, MICHAEL C

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND TITLE OF INVENTION: PACE 4.1 GENE AND POLYPRETIDES IN CELLS NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS: ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREEL FIVE PALO ALTO SQUARE

STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
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11.7%; Score 179; DB 2; Length 969;
Best Local Similarity 23.3%; Pred. No. 1.2e-07;
Matches 56; Conservative 23; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLOPPY disk
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,941
FILING DATE: 2 August 1994
ATTORNEY/AGRYT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: GLIR-009/01US
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELERCOMMUTCATION INFORMATION:
                                                                                                    ---VSIVHCEAS----EWS---
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TELEPAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INPORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-447-642-2
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US-08-447-642-2
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APPLICANT: Barr, Philip J
APPLICANT: Kiefer, Michael C
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Polypeptides in Cells
FILE REPERENCE: CHIR-009/04US
CURRENT APPLICATION NUMBER: US/09/236,503
CURRENT PILING DATE: 1999-01-25
EARLIER FILING DATE: 1994-08-02
EARLIER FILING DATE: 1994-08-02
EARLIER FILING DATE: 1994-08-02
EARLIER APPLICATION NUMBER: 07/848,629
EARLIER FILING DATE: 1992-03-09
WUMBER OF SEQ ID NOS: 16
159 CMKKGKTC----GFKRG-----TBTRVRDILQHPSAKGKGNLCPPTSBTRTCIVQRK 206
                          737 YPGDTAARRCRR-----CHKGCBTCSSRAATQCLSCR-RGFY-----HHQEMNT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 ANNHIMEC------PWSP 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NFCTKCKSGPYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         898 CRRCDENCLSCAGSSRNCSRCKTGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--RRK 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFFVLBRIGMKQIGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 179; DB 3; Length 969; 23.3%; Pred. No. 1.2e-07; tive 23; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      Sequence 2, Application US/09236503
Patent No. 6277590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 23.34
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-503-2
                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94306
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                                                                                                                             US-09-236-503-2
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799 amino acids
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-368-852-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-525-940-23
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CITY: De
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NFCTKCKSGFYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780 CVTLCPAGPYADE--SQKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838 PDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWRCVPACGEGFYPEEMPGLPHKV 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 CMKKGKTC----GPKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 YIGSQNASRGRRORRMHPNVSQGCQGCCATCSD--YNGCLSCKPRLFFVLERIGMKQIGV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08368852;
Patent No. 569183;
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMFHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 ANNHTMBC------WSIVHCBAS----EWS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,852
FILING DATE: 05-JAN-1995
CLASSITATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Verser, Carol Talkington
Patentin Release #1.0, Version #1.25
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
REPERENCE/DOCKET NUMBER: GHIR-009/00US
TELEPHONE: (415) 494-7622
TELEPRA: (415) 494-7622
TELEPRA: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.7%; Score 179; DB
Best Local Similarity 23.3%; Pred. No. 1.2e-
Matches 56; Conservative 23; Mismatches
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    : 969 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 80203
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SOPTWARE:
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93 NKCTKCKVDCDTCPNK--NPCTKCKSGPYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 148
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                                                                                                                                                                                                                                                                                                                                                                                                                             35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLPFVLBRIGWKQIGVCLSSCPSGYYGTRYPDI 92
                                                                                                                                                                                                                                                                                                                                                                                 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 BASEWSPWSPCMKKGKTC-GPKRGTETRVRDILQHPSAKGKGNLCPPTSB 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 ------RKCSENXKTCTBFHXCTBCRDGLSLQ------GSRCSVSCB 147
                                                                                                                                                                                                                                                                                                                            DB 1; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08525940

Patent No. 5866351

GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
ATTLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
ATTLE OF INVENTION: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                              57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                            ; Score 155; DB 1; 
; Pred. No. 4e-06; 
23; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
RILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 37,459
RESTRENCE/POCKEY NUMBER: 2648-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                            10.1%;
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TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
                                                                                         TELEPAK: 303/863-0223
INPORMATION POR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.2%
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149 EASEWSPWSPCMKKCKTC-GFKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                               STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                    CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-08-976-838-21
                                                                                                                            US-08-525-940-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 NKCTKCKVDCDTCFNK--NFCTKCKSGFYLH--LGKCLDSCPEGLRANNHTMECVSIVHC 148
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                                                                                                                                                                35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDI 92
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                                                                                                                                                                                                                                                                                                                                                 ------RKCSENCKTCTEFHNCTECRDGLSLO-----GSRCSVSCE 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08976838
Patent No. 5981259
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION:
OF INVENTION:
MUMBER OF SEQUENCES:
ADDRESSER:
ADDRESSER:
Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                        10.0%; Score 154; DB 2; Length 799; 28.2%; Pred. No. 1.6e-05; Live 23; Mismatches 57; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION UNMBER: US/08/976,838
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 154; DB 2; 28.2%; Pred. No. 1.6e-05; tive 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2848-11-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2848-
TELECOMMUNICATION INFORMATION:
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-973
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE GHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
                                                                                                                                48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-838-23
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denver
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-976-838-23
                                                       US-08-525-940-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: I
STATE:
                                                                                                                                                                                                                                                                                                                                                   624
                                                                                                                                Matches
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606 PECSEVGCDGPGPDHCND---CL----HYYYKLK----NNTRICVSSCPPGHY---HADK 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 KRCKKCAPNCESCFGSHGDQCMSCKYGYFLNBETNSCVTHCPDGSYQDTKKNLC----- 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 PNVSQ-GCGG-GCATCSDYNGCISCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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|: | : |
------GSRCSVSCB 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 881;
                                                                                                                                                                                                                           APPLICANT: Franciscoff, Alex
APPLICANT: Miranda, Iuis R.
APPLICANT: Miranda, Iuis R.
APPLICANT: Wolf, JOSEPH R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.0%; Score 154;. DB 2; 28.2%; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Mismatches
                ------RKCSENCKTCTEFHNCTECKDGLSLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIPTIONIN: 514
PRIOR APPLICATION DATA:
APPLICATION UDMER: US 08/368,852
FRIOR APPLICATION DATA:
FRIOR APPLICATION DATA:
APPLICATION WIMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION WUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               Sequence 21, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
US-08-525-940-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 NKCTKCKVDCDTCFNK--NPCTKCKSGFYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; Indels 42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RKCSENCKTCTEPHNCTECRDGLSLQ-----GSRCSVSCE 740
                                           GENERAL INFORMATION:
APPLICANT:
PRAIZUSOFÉ, Alex
TITLE OF INVENTION: CD4 T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.0%; Score 154; DB 2; Length 881;
Best Local Similarity 28.2%; Pred. No. 1.8e-05;
Matches 48; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08525940
Sequence 18, Application US/08525940
Batent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 2848-11-C2
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-923
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                             ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 21, Application US/08976838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-976-838-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                        STATE: Colorado
                                                                                                                                                                                                                                                                                                 U.S.A.
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                                                                                                                                                                                                                                                                                                                      80203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                              Query Match 10.0%; Score 154; DB 2; Length 915; Best Local Similarity 28.2%; Pred. No. 1.9e-05; Matches 48; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 154; DB 4; Length 915; 28.2%; Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLEO PE INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILLE REFERENCE: PRO-PROTEIN CONVER ENZ
CURRENT PILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR PILING DATE: 1996-07-26
PRIOR PILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOPTWARE: PARCENTIN VOIC: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Conservative 23; Mismatches
                                                     2848-11-C2
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NAME: Connell, Gary J.
REGISTRATION UNUBER: 32,020
REFERENCE/DOCKET NUBBER: 2848:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
INPORMATION POR SEQ ID NO: 18:
SEQUENCE STRANSTICS:
LENGTH: 915 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-976-838-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQ ID NO 2
; LENGTH: 915
; TYPE: RRT
; ORGANISM: Homo sapiens
US-09-214-5558-2
                                                                                                                                                                                                                                              linear
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Best Local Similarity
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US-09-214-555B-7
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640 PECSEVGCDGPGPDHCND----CL----HYYYKLK----NNTRICVSSCPPGHY----HADK 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Indels
GENERAL INPOMATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILLE REFERANCE: PRO-PROTEIN CONVER ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT PILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
FRIOR APPLICATION NUMBER: 2,203,745
FRIOR APPLICATION NUMBER: 2,203,745
FRIOR PILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN OF: 2.1
SEQ ID NO 7
LENGTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 154; DB 4; 28.2%; Pred. No. 1.9e-05; tive 23; Mismatches 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
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APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
10S-08-525-940-15
Sequence 15, Application US/08525940
Patent No. 5866351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.2
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colorado
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LITY: Denver
STATE: Col
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CITY: De
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Frazusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   Query Match 9,9%; Score 152; DB 2; Length 288; Best Local Similarity 27.7%; Pred. No. 7.4e-06; Matches 48; Conservative 24; Mismatches 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Derver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PETENTY APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REBERRENCH/OCCET NUMBER: 2848-11-C2
TELECOMUNICATION INFORMATION:
TELEPAN: (303) 863-9700
TELEPAN: (303) 863-9700
INPORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 aminia acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                          TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-023
INPORNATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                : 288 amino acids
amino acid
                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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Best Local Similarity
Matches 48; Conserva
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US-08-976-838-15
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35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDI 92

48; Conservative

48; Gaps

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S9 KRCRKCAPNCESCFGSHGDQCMSCKYGYFLNEETNSCVTHCPDGSYQDTKKNLC----- 112
                                                                 93 NKCTKCKVDCDTCFNK--NPCTKCKSGFYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 148
13 PECSEVGCOGPGPDHCND---CL---HYYYKLK----NNTRICVSSCPPGHY---HADK 58
                                                                                                                                                                              149 EASEWSPWSPCMKKKKTCGFKRGTE----TRVRDILQHPSAKGKGNLCPPTSE 197
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Job time : 14.5595 secs
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Sequence Seq

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US-09-894-912A-14
US-10-125-852-18
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US-10-125-852-24
US-09-84-912A-25
US-09-84-912A-25
US-10-108-260A-4829
US-10-118-770-2
US-10-125-852-13
US-10-125-852-13
US-10-125-852-15
US-10-125-852-15

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	OR PILING DATE	DATE:	2001-01-09	-09									
	PRIOR APPLIC		NUMBER:	60	543,7	774							
	FIE	E i	3: 2000-04	-05									
	NUMBER OF SEC	10.10	ID MOS: 46 ont In version	۳									
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 28110/37260A
CURRENT APPLICATION NUMBER: US/09/894,912A
CURRENT PILING DATE: 2001-05-10
PRIOR PRIOR APPLICATION NUMBER: 60/26,614
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-06-28
PRIOR PLICATION NUMBER: 09/757,562
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 48
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; Sequence 34, Application US/09894912A

US-09-894-912A-34

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Sequence 23, Application US/10125852

Sequence 23, Application US/10125852

Publication No. US20030032034A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-1

TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES

FILE REFERENCE: HYS. 43A

CURRENT APPLICATION NUMBER: US/10/125,852

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: US 60/316,368

PRIOR PILING DATE: 2001-08-30

PRIOR PILING DATE: 2001-08-30

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE PATENTION NUMBER: 13

LENTH: 272
APPLICANTION:
APPLICANTION:
APPLICANT: Tang et al.
TITLE OF INVENTION: BETHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: BETHODS AND POLYBEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 28110/37260A
CURRENT APPLICATION NUMBER: US/09/894,912A
CURRENT PILING DATE: 2002-05-10
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
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US-09-894-912A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-852-23
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121 HIGKCLDNCPEGLEANWHTMECVSIVHCEVSEWNPWSPCTKTGKTCGFKRGTETRVREII 180
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183 HPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKE--AIPDSKS 238
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9
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Treacy, Maurice
Spaulding, VikM.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 292;
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ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE PATENTIAN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/745,763

FILING DATE: 18-Jun-2000

CLASSIPTCATION: <a href="https://doi.org/10.100/10.100/">CLASSIPTCATION: <a href="https://doi.org/10.100/">CLASSIPTCATION: <a href="https://doi.org/10.100/">ATTORNEY/AGENT INFORMATION: <a href="https://doi.org/10.100/">ATTORNEY/AGENT INFORMATION: <a href="https://doi.org/10.100/">ATTORNEY/AGENT INFORMATION: <a href="https://doi.org/10.100/">DIATORNEY/AGENT INFORMATION: <a href="https://doi.org/">DIATORNEY/AGENT INFORMATION: <a href="https://doi.org/">DIA
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                                                                                         84.2%; Score 1293; DB 9;
85.1%; Pred. No. 2.6e-95;
iive 14; Mismatches 21;
                                                                  242 LESSIETPDOQENKERQQQQKRRARDKQQKSVSVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-745-763-166
                                                                                                                                                                                                                                                                                                                                                                                                                McCoy, John M.
LaVallie, Edward R.
Colling-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  Sequence 166, Application US/09745763 Patent No. US20020065394A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 498-8284
TELERAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 166:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 292 amino acids
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jacobs, Kenneth
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Best Local Similarity 85.11
Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                           US-09-745-763-166
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Sequence 13, Application No. US20030044792AI

GENERAL INFORMATION:
APPLICANT: Tang et al.
TITLE OF INVENTION:
FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPRENCE: 28110/37260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: To be assigned
PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-38

PRIOR PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patent In version 3.0

SEQ ID NO 9.13
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                                                                                                   7; Gaps
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                                 85.7%; Score 1315.5; DB 14; Length 272; 87.1%; Pred. No. 3.8e-97; Live 11; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 SLESSKRIPBQRENK--QQQKKRKVQDK-QKSVSVSTVH 272
                                    Query Match 85.7% Best Local Similarity 87.1% Matches 243; Conservative
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Matches 242; Conservative
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ORGANISM: Homo sapiens
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Sequence 26, Application US/09894912A

Sequence 26, Application No. US20030044792A1

Fublication No. US20030044792A1

GENERAL INPORMATION:

APPLICANT Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILER REFERENCE: 28110/37260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT PILING DATE: 2002-05-10

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-65

PRIOR PILING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.2%; Score 1293; DB 14; Best Local Similarity 85.1%; Pred. No. 2.6e-95; Matches 235; Conservative 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GLESSIETPDQQENKERQQQXRRARDKQQKSVSVS 276
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86.7%; Pred. No. 1e-94;
tive 12; Mismatches 18;
                                                         09/799,451
PRIOR FILING DATE: 2001-08-30
PRIOR PRILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE Patentin version 3.1
SEQ ID NO 25
LENGTH: 292
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Best Local Similarity 86.7%
Matches 234; Conservative
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US-10-125-852-25
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US-09-894-912A-26
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Publication No. US20030032034A1
GENERAL INFORMATION:
ATTLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-1
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF TATLE OF 
                                                                                                                                                                                                                                                                                                                                                                   US-09-894-912A-48

US-09-894-912A-48

Sequence 48, Application US/09894912A

Publication No. US2030044792A1

GENERAL INPORMATION:

APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH

TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES

FILE REFERENCE: 28110/37260A

CURRENT APPLICATION NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: To 2002-05-10

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-06-28

PRIOR PLILING DATE: 2000-06-28

PRIOR PLILING DATE: 2000-06-28
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          181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKB--AIPDSK 236
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84.2%; Score 1293; DB 10; Length 292;

Best Local Similarity 85.1%; Pred. No. 2.6e-95;

Matches 235; Conservative 14; Mismatches 21; Indels 6
                                                                                                                                                  SLESSKEI PEQRENK -- QQQKKRKVQDKQKSGIBVT 270
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PRIOR APPLICATION NUMBER: US 60/316,368
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US-10-125-852-25
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Sequence 4, Application US/10185770
Publication No. US20030022217A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THERROF
FILE REPERENCE: CL0001247
CURRENT APPLICATION NUMBER: US/10/185,770
CURRENT PILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/301,852
NUMBER OF SECRETE OF 100-07-02
NUMBER OF SECRETE OF 100-07-02
NUMBER OF SECRETE OF MINDOR Version 4.0
SECIENCE OF THE OFFICE OFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 225;
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Pred. No. 8.6e-83;
6; Mismatches 14; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Past Local Similarity 92.5%; Pred. No. 5.7e-87;
Matches 210; Conservative 5; Mismatches 10; Indels
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Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David N.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: NOVEL CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: 000 CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: 000 CCMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: 000 CCMPOSITIONS AND METHODS FOR

FILE OF INVENTION NUMBER: US/10/087,192

CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1782
LENGTH: 239
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Best Local Similarity 90.1%;
Matches 201; Conservative 6
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US-10-087-192-1782
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US-10-087-192-1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 225
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TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFRERNCE: 28110/37260A

CURRENT FILING DATE: 2002-05-10

PRIOR FILING DATE: 2002-05-10

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 48

SOFTUME OF SEQ ID NOS: 48

SEQ ID NO 16

FORCE.
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                                                61 LPFALERIGHKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                                                                                                                    HLGKCLDSCPEGLEANNHIMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                      QHPSAKGKGNLCPPTSETRTC1VQRKKCSKGERGKKGRERKRKKLNKEERKETSSSSDSK 240
                                                                                                                                                                                                                                                                                                                         181 QHPSA--KGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKKPNKGESKE--AIPDSK 236
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Best Local Similarity 86.8%; Pred. No. 9.3e-90;
Matches 224; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       241 GLESSIETPDQQENKERQQQQKRRARDKQQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 16, Application US/09894912A; Publication No. US20030044792A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-185-770-4
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Gaps

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APPLICANT: Zhong, Mei TITHE OPLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET TITHE OP INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET FILE REPERENCE: 21402-290 B CURRENT APPLICATION NUMBER: US/10/094,886 CURRENT FILING DATE: 2002-03-07 PRIOR APPLICATION NUMBER: 60/274,322 PRIOR PILING DATE: 2007-03-02
                                                                                                                                                                                                                                                                                                                                                                                                              117 GFYLHLGKCLDSCPRCLEANNHTMECVSIVHCEASEWSPWSPCHKKGKTCGFKRGTETRV 176
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                                                                                                                                                                                                                                                                                                                                     1 MHLRLISCPFIIINPMEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                                                                                            10; Indels
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Best Local Similarity 90.4%; Pred. No. 5.4e-80;
Matches 197; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/288,052
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Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
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Rastelli, Luca
Spaderna, Steven
LaRochelle, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, Li
Gorman, Linda
Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
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APPLICANT: Tchernev, Vellzar T
APPLICANT: Liu, Kiaohong
APPLICANT: Spycek, Kimberly A.
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Gusev, Vladimir
Smithson, Glennda
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Burgess, Catherine
Vernet, Corine A.
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Gerlach, Valerie
Pochart, Pascal
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NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 172
LENGTH: 239
TYPE: PRT
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                                                                                                                                 ORGANISM: Homo sapiens
US-10-094-886-172
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US-10-094-886-176
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                                                                                                                              HIGKCLDSCPEGLERNNHTWECVSIVHCEASEWSPWSPCWRKGKTCGFKRGTETRVRDIL 180
                      LPPVLBRIGHKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTGFNKNPCTKCKSGFYL 120
                                                                                                                                                                Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                          181 OHPSAKGKGNICPPISETRICIVORKKCSKGERGKKGRERKRK 223
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PRIOR APPLICATION NUMBER: 60/274, 322
PRIOR FILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-05
PRIOR PILING DATE: 2001-05-05
PRIOR PILING DATE: 2001-05-05
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
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Padigaru, Muralidhara
Taupier, Raymond J., Jr.
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Liu, Xiaohong
Spytek, Kimberly A.
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Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
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Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
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Burgess, Catherine
Vernet, Corine A.
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Rastelli, Luca
Spaderna, Steven
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Pochart, Pascal
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Casman, Stacie
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APPLICANT:
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US-10-094-886-174
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                             PRIOR APPLICATION NUMBER: 60/318,510
FRIOR FLING DATE: 2001-09-10
FRIOR PLING DATE: 2001-09-10
FRIOR PLING DATE: 2001-03-08
FRIOR PLING DATE: 2001-03-08
FRIOR PLING DATE: 2001-08-11
FRIOR PLING DATE: 2001-08-21
FRIOR PLING DATE: 2001-03-08
FRIOR PLING DATE: 2001-03-09
FRIOR PLING DATE: 2001-06-07
FRIOR PLING DATE: 2001-06-07
FRIOR PLING DATE: 2001-06-07
FRIOR PRIOR PLING DATE: 2001-08-21
FRIOR PLING DATE: 2001-08-21
FRIOR PLING DATE: 2001-08-21
FRIOR PLING DATE: 2001-08-21
FREMAINING PRIOR APPLICATION NUMBER: 60/313,626
FREMAINING PRIOR APPLICATION APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.1%; Score 1045; DB 15; Length 195; 92.8%; Pred. No. 1.1e-75;
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Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Burgess, Catherine
APPLICANT: Li, Li, Li, APPLICANT: Li, Li, Li, APPLICANT: Gorman, Linda
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Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
Shenoy, Suresh
Padigaru, Muralidhara
Taupier, Raymond J., Jr.
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Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 TCIVQRKKCSKGERG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 KCTVORKKCOKGERG 193
FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 92.8
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller, Charles
Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-094-886-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT:
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APPLICANT: LANCORDELE, WALLILDON,
APPLICANT: ANDOROGUELE, WALLILDON,
ITILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.
ITILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.
ITILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.
ITILE OF ILLNG DATE: 2002-03-07
PRIOR PLILING DATE: 2001-03-07
PRIOR PLILING DATE: 2001-03-10
PRIOR PLILING DATE: 2001-03-10
PRIOR PLILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-06-07
PRIOR PLING DATE: 2001-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGPYLHLGKCLDNCPEGLEANNHT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 MECVSIVHCBASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKGKGNLCPPTSETR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 MECYSIVHCEVSERNPWSPCTKKGKTCGFKRGTETRVREIIQHPSA--KGNLCPPTNETR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GSQNASRGRRQRRWHPNVSQGCRGGCATCSDYNGCLSCKPRLFFALBRIGMKQIGVCLSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFVLBRIGMKQIGVCLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 29, 2004, 17:15:57
Job time : 37.5837 secs
Pernandes, Elma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 TCIVQRKKCSKGERG 214
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 29, 2004, 16:56:05; Search time 14.2209 Seconds (without alignments) 1887.186 Million cell updates/sec

Title: Perfect score:

US-09-894-912A-32 1535 1 MHLRLISCPFIILNFMEYIG......QQKRRARDKQQKSVSVSTVH 279 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	serine proteinase	furin (BC 3.4.21.7	subtilisin-like pr	subtilisin-like pr	subtilisin-like pr	furin (BC 3.4.21.7	PACE4A - mouse (fr	protein bli-4D [im	probable proprotei	subtilisin-like pr	probable kexin (EC	gene PACB4 protein	subtilisin-like pr	subtilisin-like pr	insulin-like growt	F-spondin precurso	cell-fate determin	F-spondin - rat	Motch B protein -	Wnt inhibitory fac	insulin-like growt	Xotch protein - Af	Wnt inhibitory fac	hypothetical prote	hypothetical prote	protein-tyrosine k			insulin receptor (
SUMMARIES	OI	S34583	T43251	A39490	JC5571	JC5570	A43434	152527	D87803	B48225	.A48225	T37314	153282	G02428	JC6148	A33837	A47723	A49128	A38152	A49175	B59180	IGHUR1	A35844	A59180	T24232	T27283	S70713	B47417	B36502	S57245
	DB	2	7	-	~	7	~	7	~	~	-	~	7	~	N	N	7	~	7	N	0	Н	N	N	~	N	~	~	N	7
	* Query Match Length	1548	1299	696	962	975	1680	932	942	915	915	570	937	899	915	1371	803	2471	807	1203	378	1367	2524	379	440	1620	1369	540	1268	2101
•	Query Match	12.2	12.1	11.7	11.4	11.4	11.3	11.1	11.1	10.7	10.7	10.6	10.5	10.0	10.0	9.7	9.5	9.4	9.3	9.5	9.1	9.1	9.1	9.0	B.9	9.9	B.9	8.7	8.5	8.5
	Score	187	185.5	179	174.5	174.5	174	171	170.5	164	163.5	162	161	154	154	149	145.5	144.5	142.5	140.5	140	139.5	139	138.5	137	137	136.5	133	131	131
	Result No.	1	7	m	4	'n	v	7	80	on	10	11	12	13	14	15	16	17	18	19	20	21	. 22	23	24	25	56	27	28	29

ingulin receptor -	insulin receptor p	notch protein homo	notch-1 protein -	inBulin receptor p	ingulin receptor p	transmembrane prot	notch protein homo	hypothetical prote	tumor necrosis fac	furin (BC 3.4.21.7	trophozoite cystei	cysteine rich prot	trophozoite surfac	insulin receptor-r	probable transform
A56081	INHUR	S18188	A46019	A34157	A36080	S42612	A40043	T26972	JC4302	843656	C42125	T42017	A48579	A36502	826059
-	-	~	~	ď	N	~	~	~	N	N	~	~	~	~	7
2148	1382	2531	2531	1372	1383	2437	2555	1111	461	837	677	1274	667	1300	375
8.5	8.5	8.5	8.5	8.4	8.4	8.4	8.4	9.4	8.3	8.5	8.2	8.2	8.1	8.1	8.0
131	130.5	130	130	129.5	129.5	129	129	128.5	128	126.5	126	125.5	124.5	124	123.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 2 T43251

furin (BC 3.4.21.75) - fall armyworm
NiAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase; sering
Cispecies: Spodoptera frugiperda (fall armyworm)
Cispecies: Spodoptera frugiperda (fall armyworm)
Cispecies: Spodoptera frugiperda (fall armyworm)
Cispecies: Tail 1. Jan. 2000
Cis

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subtlisin-like proprotein convertase (BC 3.4.21.-) PACB4 precursor, splice form E-II - C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JC5571
R; Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Ni A; Ticle: A novel human PACB4 isoform, PACB4E is an active processing protease containing A; Reference number: JC5570; MUID:97335942; PMID:9192737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CjAccession: JG5570
RjMori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Ni
Biochem. 121, 941-948, 1997
A;Title: A novel human PACR4 isoform, PACR4E is an active processing protease containing
A;Reference number: JC5570; MUID:97335942; PMID:9192737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: brain cerebellum C;Comment: This enzyme is a processing protease and responsible for processing of varion ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilisin-like proprotein convertase (BC 3.4.21.-) PACB4 precursor, splice form E-I
C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Bxperimental Bource: brain cerebellum
C,Comment: This enzyme is a processing protease and responsible for processing of
ch it is retained intracellularly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825 PDSBLIRCGECHITCGTCVGPGREECIHCARNFHFHDWKCVPACGEGFYPREMPGLPHKV 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: DDBJ:D87994; NID:g2330550; PIDN:BAA21792.1; PID:g2330551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: DDBJ: D87993; NID: 92330548; PIDN: BAA21791.1; PID: 92330549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGFYLHLGKCLDSCPEGLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YIGSQNASRGRRQRRMHPNVSQGCQGCCATCSD--YNGCLSCKPRLFFVLERIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Superfamily: subtilisin-like proteinase proteinase
C;Keywords: glycoprotein; hydrolase; serine proteinase
E;1-62/Domain: signal sequence #status predicted <PRO>
F;196-434/Domain: propeptide #status predicted <PRO>
F;196-434/Domain: subtilisin homology <PRO>
F;398-954/Domain: hydrophobic cluster #status predicted <PGL>
F;205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 CMKKGKTCGPKRGTETRV-----RDILQHPSAKGKGNLCPPT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRRYGPPGGERQATVSSKGVPGGQSLSASSPGAGEGMLHHPT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%; Score 174.5; DB 2 23.9%; Pred. No. 0.00045; tive 25; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-962 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
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A; Residues: 1-975 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC5570
                                                                                                                                                                                                                                                                                                                                                           A; Accession: JC5571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Genetics:
A,Gene: GDB:PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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A; Residues: 1-1299 <CIE>
A; Cross-references: EMBL: Z68888; NID: g1167859; PID: e219690; PIDN: CAA93116.1
A; Experimental source: clone Sfurin 6; ovary
C; Function:
A; Description: responsible for the endoproteolytic processing of proproteins with specif C; Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlternate names: kexin homolog
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 10-Sep-1999 #text_change 31-Mar-2000
C;Accession: A39490
R;Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A;Reference number: A39490; MUID:92075167; PMID:1741956
A;Accession: A39490
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                 -----VSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGPYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 ANNHTMEC------PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               898 CRRCDENCLSCAGSSRNCSRCKTGFTQLGTSCITNHTCSNADETPCBMVKSNRLC--ERK 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 PDSELIRCGECHHTCGTCVGPGREECIHCAKNFHFHDWKCVPACGEGFYPEEMPGLPHKV 897
                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLPFVLERIGMKQIGV 75
                                                                                                                                                                                                                                                                                                                                                              36 NVSQGCQGGCATCSD-YNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-969 «KIE»
A;Cross-references: GB:M80482; NID:g189531; PIDN:AAA59998.1; PID:g189532
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTKCKVDCDTCP--NKNPCTKCKSGPYLHLGKCLDSCPEGLBANNHTMEC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 15q26-15q26
C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Superfamily: subtilisin-like proteinase PACE4; serine proteinase
F;150-969/Product: serine proteinase PACE4 #status predicted <81G>
F;196-434/Domain: subtilisin homology <8ET>
F;196-434/Domain: subtilisin homology <8ET>
P;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    904 TSAFCLSCEPKWELNKKGKCMPVGSDKCSAGEFAVDQKCKRCNPACDSCYGEN-
                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                DB 2; Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 179; DB 1; Length 969; 23.3%; Pred. No. 0.00023; Live 23; Mismatches 89; Indels
                                                                                                                                                                                                                             ch 12.1%; Score 185.5; DB 2; Length 1
1 Similarity 24.5%; Pred. No. 0.00011;
54; Conservative 24; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 QHPSAKGKGNLCPPTS -- ETRTCIVQRKKCSKGERGKKGR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9/
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Matches
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Directin bli-4D [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
C;Accession: D87803
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID: 99065813; PMID: 99551916
A;Reference number: A55000; MUID: 99065813; PMID: 99551916
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                             C;Accession: 152527 K.; Nakayama, K. R;Hosaka, M.; Murakami, K.; Nakayama, K. Biomed. Res. 15, 383-390, 1994 B;Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801 PDSELVKCGECHHTCRTCVGPSREBCIHCAKSPHPQDWKCVPACGEGFYPBEMPGLPHKV 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861 CRRCEENCLSCEGSSRNCSRCKAGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674 NCHDECNGCTESSSATSCPACK-HLTQTLRNXGGSGP-KCVQKCDDTY----YLDGDKC 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                 PACE4A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGPYLHLGKCLDSCPEGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMKKGKTC----GPKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 YFGDAAARRCRR------HHQETNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:chr_I; PIDN:AAB96754.1; PID:g2773243; GSPDB:GN00019
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 NVSQCCQGCCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:D50060; NID:g769700; PIDN:BAA08777.1; PID:g769701
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
P;172-410/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 171; DB 2; Length 932; 22.9%; Pred. No. 0.00073; tive 25; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 170.5; DB 2; Length 328.3%; Pred. No. 0.0008; tive 18; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VSIVHCBAS----EWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: 152527
A,Status: preliminary; translated from GB/EMBL/DDBJ
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                             ---PCOEGCKTC 1170
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Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: I52527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-932 < RES>
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A;Molecule type: DNA
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                                1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             furin (BC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cipaces: Or-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
CiAccession: A44344
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, B. A. Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein prodA;Reference number: A4334; MUID:92381036; PMID:1512259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 NKCTKCKVDCDTCF--NKNFCTKCKSGFYLHLGKCLDSCPEGLEANNHTMECVSIVHCEA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NPCTKCKSGFYLHLGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 ANNHTMEC------PSIVHCEAS----EWS-----PWSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         838 PDSBLIRCGECHHTCGTCVGPGRBECIHCAKNFHFHDWKCVPACGBGFYPBBMPGLPHKV 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
                      A.Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Superfamily: subtilisin-like proteinin; hydrolase; serine proteinase
F;1-62/Domain: signal sequence #status predicted <PRO>
F;63-149/Domain: propeptide #status predicted <PRO>
F;95-494/Domain: propeptide #status predicted <PRO>
F;95-968/Domain: pubtilisin homology <SBT>
F;95-968/Domain: hydrophobic cluster #status predicted <PRO>
F;25-968/Domain: propeptide #sp. His, Asn, Ser #status predicted
F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSD--YNGCLSCKPRLPFVLERIGMKQIGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A43434
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16808A
A;Residues: 1-16808A
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
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                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%; Score 174; DB 2; Length 1680; ilarity 24.5%; Pred. No. 0.00073; Conservative 15; Mismatches 61; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: PlyBase: PBgn0004598
C,Superfamily: subtilisin homology
C,Keywords: hydrolase; serine proteinase; transmembrane protein
P;409-652/Domain: subtilisin homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                             81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 CMKKGKTCGFKRGTETRV-----RDILQHPSAKGKGNLCPPT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 11.4%; Score 174.5; DB 2 al Similarity 23.9%; Pred. No. 0.00045; 53; Conservative 25; Mismatches 81
Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 SEWSPWSPCMKGKTC 166
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 SSCPSGYY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: PlyBase:Pur2
                                                                                                                                                                                                                                                                                                                                                  Query Match
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A; Reference number: JX0248; MUID: 93224489; PMID: 8468318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-570 < THA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: | | 1
780 NGH--DC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetica
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
Cispecsion: A48225; JV0248
Riusson, J; Vieau, D; Hamelin, J; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A; Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop A; Recession: A48225
A; Recession: A48225
A; Status: preliminary
A; Mouse in Proc. Musculus (Musculus in Proc. Musculus in Musculus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lusson, J; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G. Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop A;Reference number: A48225; MUID:93342056; PMID:8341687
A;Accession: B48225
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **Reywords: duplication; glycoprotein; hydrolase; integrin binding; serine proteinase; 1.34/Domain: signal sequence #status predicted <SIG>; 1.34/Domain: signal sequence #status predicted <SIG>; 1.35-915/Product: probable proproprotein convertase 5 #status predicted <PRO>; 1.17-915/Product: probable proproteins convertase 5 #status experimental <MAT>; 1.17-915/Product: subtilisin homology <SET>; 1.17-915/Product = Nap, His, Ser #status predicted
-----HL--GKCLDSCPEGLEANNHTMECVSIV 146
                                           683 ADKKRCRKCAPNCESCFGSHADQCLSCRYGYFLNBETSSCVAQCPEGSYQDIKKNIC--- 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR-----ICVSSCPPGHF---H 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 PDINKCTKCKVDCDTCPNKNP--CTKCKSGPYLH--LGKCLDSCPEGLEANNHTMECVSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: PCS precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 23-Feb-1997
C;Accession: B48225
                                                                                                                                                               147 HCBASEWSPWSPCMKKGKTCGFKRGTETRVRDILLQHPSAKGKGNLCPPTSETRTC--IVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 VHCEASEWSPWSPCMKKGKTC-GFKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GKCSENCKTCTGFHNCTECKGGLSLQ------GSRCSVTCB 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNÅ
A;Residues: 1-915 -4103-
A;Cross-references: GB:L14933
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable proprotein convertase (BC 3.4.21.-) 5 precursor - rat
96 TKCKVDCDTCFNKNPCTKCKSGPYL-
                                                                                                                                                                                                                                                                                                                              205 RKKCSKG 211
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C;Accession: T37314
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.
R;Thacker, C.; Peters, K.;
Senes Dev. 9, 956-971, 1995
A;Title: 10-018 of Caenorhabditis elegans encodes structurally distinct kex2/sn A;Reference number: 221679; MUID:95293228; PMID:7774813
A;Accession: T37314
A MOLECULE TYPE: MRNA
A; Residues: 1-915 - KNRA
A; Residues: 1-915 - KNRA
A; Residues: 1-915 - KNRA
A; Cross-references: DDBJ: D12619; NID: g220565; PIDN: BAA02143.1; PID: g220566
A; Note: the authors translated the codon GGC for residue 915 as Ala
C; Superfamily: subtilisin-like proteinase PACR4; subtilisin homology
C; Superfamily: subtilisin-like proteins e PACR4; subtilisin homology
F; Reywords: duplication; glycoprotein; hydrolass; integrin binding; serine proteinase
F; 1-34/Domain: signal sequence #status predicted <PRO>
F; 1-34/Domain: propeptide #status predicted <PRO>
F; 11-915/Product: proprotein convertesse PC5 #status experimental <MAT>
F; 164-402/Domain: subtilisin homology <PRO>
F; 164-402/Domain: subtilisin homology <PRO>
F; 173, 214, 388/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 SSCPSGYYGTRYPDINK -- CTKCKVDCDTCFNKNFCTKCKSGFYLHLGKCLDSCPEGLEA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 Y----YLDGDKCKOKCSSKCHTCTKAEVCETCPGSLLLIDVDNMPHYDHGKCVESCPPGLV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 YYGTRYPDINKCTKCKVDCDTCFNKNFCTKCKSGFYL-----HL--GKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ANNHIMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILOHPSAKGKGNLCPP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YYINAVGKCDLCDS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable kexin (BC 3.4.21.61) - Caenorhabditis elegans (fragment)
N;Alternate names: blisterase 4
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 RSSPPDLTSGWKLSCDECNGGCTESSSATSCFAYK-HLTOTLRNKGGSGF-KCVOKCDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFVLBRIGMKQIGVCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.7%; Score 163.5; DB 1, Length 9:
Best Local Similarity 29.1%; Pred. No. 0.0022;
Matches 44; Conservative 18; Mismatches 50; Indels
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C;Keywords: alternative splicing; hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 NNHTMECVSIVHCRASEWSPWSPCMKKGKTC 166
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Subtributed the proprotein convertage (EC 3.4.21.-) homolog - human
N.Alternate names: PC6A protease
C.Species: Homo sapiens (man)
C.Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C.Jacesion: JC6148
R.Miranda, L.; Wolf, J.; Pichuantes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A; Prite: Isolation of the human PC6 gene encoding the putative host protease for HIV-1 gi
A; Contents: CEM F.cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin-like growth factor I receptor precursor - rat
NiContains: insulin-like growth factor I alpha chain; insulin-like growth factor I beta of
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Aar-1990 #sequence revision 03-Nov-1995 #text_change 21-Jul-2000
Cispecies: Johnar-1990 #sequence revision 03-Nov-1995 #text_change 21-Jul-2000
Cispecies: Aar-1990 #sequence revision 03-Nov-1995 #text_change 21-Jul-2000
Cispecies: Aar-1990 #sequence revision 03-Nov-1994
Ripecial M.T.; Giorgino, F.; Smith, R.J.
Apritle: cDNA cloning of the rat IGP I receptor: Structural analysis of rat and human IGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-364 KMR2.
A;Cross-references: GB:M27293
R;Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.
R;Kurachi, H.; Jobo, K.; Comun. 187, 934-339, 1992
Biochem. Biophya: Rea: Comun. 187, 934-339, 1992
A;Title: A new member of the insulin receptor family, insulin receptor-related receptor,
A;Reference number: PC1130; MUID:92412145; PMID:1530648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1.1371 <PRD>
K;Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D.
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989
A;Title: Developmental regulation of the rat insulin-like growth factor I receptor gene.
A;Reference number: A33837; MUID:90017496; PMID:2477843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-915 <MIR>
A;Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C;Comment: This protein functions as a soluble enzyme within the secretory pathway. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 PNVSQ-GCQG-GCATCSDYNGCLSCKPRLPPVLERIGMKQIGVCLSSCPSGYYGTRYPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 PECSEVGCDGPGPDHCND---CL---HYYYKLK----NNTRICVSSCPPGHY---HADK
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C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase
P;164-402/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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149 BASEWSPWSPCMKKGKTC-GPKRGTETRVRDILQHPSAKGKGNLCPPTSE
                                  DB 2; Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels
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A;Accession: JC2461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 154; DB 2; 28.2%; Pred. No. 0.009; tive 23; Mismatches E
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                                                            724
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R;Johnson, R.C; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.E.
Endocrinology 135, 1178-1185, 1994
A;Title: PACE4: a subtliisin-like endoprotease prevalent in the anterior pituitary and A;Reference number: 153282; MUID:94349873; PMID:8070361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC 3.4.21.-) 5 precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNK-NFCTKCKSGFYLALGKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      806 PDSELIRCGECHHTCRTCVGPSREECIHCARSFHPQDWKCVPACGEGFYPEEMPGLPHKV 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           966 CRRCDENCLSCEGSSRNCSRCKAGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 PRCSEVGCDGPGPDHCND---CL----HYYYKLK----NNTRICVSSCPPGHY---HADK 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G02428
subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fra C; Species: Homo sapiens (man)
C; Species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
                                                                                               Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 YIGSONASRGRRORRMHPNVSQGCQGCCATCSDYN--GCLSCKPRLFFVLBRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CMKKGKTC----GPKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:L31894; NID:g496221; PIDN:AAA61987.1; PID:g496222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology P;177-415/Domain: subtilisin homology <SBT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 10.5%; Score 161; DB 2; Length 937; Local Similarity 22.5%; Pred. No. 0.0032; Lengthe 54; Conservative 24; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                          A;Accession: I53282
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-937 <RES>
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A,Accession: G02428
A,Statuus: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-899 <REU>
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R;Reudelhuber, T.L.
submitted to the EMBL Data Library, February 1996
                                                                  gene PACE4 protein - rat
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Best Local S
Matches 54
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A.Residues: 913-984, PV', 987-1017 < KUR>
A.Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359
A.Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359
A.Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359
C.Superfamily: insulin receptor; December related transforming protein; transmembr p:1-30/Domain: signal sequence #status predicted <SIG>P:1-30/Domain: signal sequence #status predicted <SIG>P:1-31-74/Product: insulin-like growth factor I beta chain #status predicted <IGA>P:742-1371/Product: insulin-like growth factor I beta Chain #status predicted <IGB>P:911-974/Region: GPXY motif
P:971-974/Region: MPXY motif
P:998-1275/Domain: protein kinase homology <KIN>P:1006-1014/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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DEVELOPMENTAL EXPRESSION.

MEDLINE-96293359; PubMed=8698813;

CONSTAM D.B., Calfon M., Robertson E.J.;

"SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis.";
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MEDLINE=97103178; PubMed=8947550;
De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
The isoforms of proprotein convertase PCS are sorted to differe subcellular compartments ";
J. Cell Biol. 135:1261-1275(1996).
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xenopus lae
homo sapien
quar musculu
giardia lam
sus scrofa
homo sapien
drosophila
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                                                                Name=PCSB; Synonyma=Long;
Name=PCSB; Synonyma=Long;
IsoId=Q04592-1; Sequence=Displayed;
Name=PCSA; Synonyma=Long;
IsoId=Q04592-2; Sequence=USP_015438, VSP_015439;
IsoId=Q04592-2; Sequence=VSP_015438, VSP_015439;
Intestine, adrenals and lung but not in the brain.

-:- DEVELOPMENTAL STAGE: Weakly expressed throughout the embryo, except in the developing nervous system, the ribs and the liver, but markedly upregulated at discrete sites during development. At B6.5, prominent expression observed in differenciated decidua. At B7.5, intense expression in extraembryonic endoderm, amnion and nascent mesoderm. At B8.5, abundant expression in somites and yolk act followed by a confination to dermamyotome compartment. Between B9.5 and B11.5, abundant expression in ARR (thickened ectodermal cells of limb buds). At B12.5, expression in the limbs is confined to the condeminal mesoner was earliage of At this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license @igreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the tongue. At 816.5, abundant expression in epithelial cells of the intestinal villi. Isoform A is most abundant at all stages but significant levels of isoform B occur at 812.5 DOMAIN: The propertide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sorting information. AC 1 directs TCN localization and interacts with the TCN sorting protein PACS-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to peptidase family SB. SIMILARITY: Contains 1 homo B/P domain.
                                     DEVELOPMENTAL EXPRESSION.
MEDLINE=97436919; Pubmed=9291583;
Cell Biol. 134:181-191(1996)
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ALTERNATIVE PRODUCTS:
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MGD; MGI:97515; PCBKS. InterPro; IPR006212; Purin repeat. InterPro; IPR009030; Grow_fac_recep.

EMBL; L14932; AAA74636.1; -

PIR; A48225; A48225. PIR; S34583; S34583. HSSP; Q99405; IMPT. MEROPS; S08.076;

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1254 SCEKCSEDCVSCSGADICQQCLSQPDNTILLHEGRCYHSCPEGFYAKDGVCE----HCS 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1209 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPQG----TWPSVTSG 1253
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InterPro; IPR000209; Peptidase S8.
InterPro; IPR002804; Peptidase S8B.
InterPro; IPR009209; Protease Inhib.
Pfam; PF00483; Proproctein; I.
Pfam; PF00483; Proproctein; I.
Pfam; PF00483; Proproctein; I.
PRINTIS; PR00723; SUBTILISIN.
R PRODOM; P0000717; P domain; I.
SWART; SW00261; FU; 22.
R PROSTTE; PS00136; SUBTILASE ASP; I.
PROSTTE; PS00137; SUBTILASE BIS; I.
PROSTTE; PS00137; SUBTILASE SRE; I.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
M Cleavage on pair of basic residues; Repeat; Alternative splicing;
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CLEAVAGE (AUTO-) (BY SIMILARITY)
CRELL ATTACHMENT SITE (POTENTIAL)
CHARGE RELAY SYSTEM (BY SIMILARI
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1877 AA; 209287 MW; EC850E2DF20BA1C3 CRC64;
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P_005439.
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CATALYTIC.
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1 Similarity 27.8%;
52; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       MEDLINE=20175281; PubMed=1070868;
A Oliva A.A. Jr., Chan S.J., Steiner D.F.;
I "Bvolution of the protormone convertases: identification of a non-logue of PC6 in the protochordate amphioxus.";
D isochim. Biophys. Acta 1477:338-348(2000)
C --- FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and requiated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif (By similarity).
C --- CATALYITY: Release of mature proteins from their proproteins by cleavage of Axy-Xaa-Yaa-ARC-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Axg or Lys.
C --- SUBCELLIULAR LOCATION: ISOPORM A AND ISOPORM C ARE SECRETED.
C --- ALTERNATIVE PRODUCTS:
                                  Q9NJ15; Q9NJ14; QNNJ16;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Proprotein convertase subtiliain/kexin type 5 precursor (BC 3.4.21.-)
(Proprotein convertase PC6-like) (aPC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=Q9NJ15-3; Sequence=VSP 005442, VSP 005443; DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
Cleavage on pair of basic residues; Repeat; Alternative splicing;
                                                                                                                                      Branchiostoma californiensis (California lancelet) (Amphioxus).
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae,
Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9NJ15-2; Sequence=VSP_005444, VSP_005445;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bvent=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006212; Furin repeat.
InterPro; IPR006030; Grow fac recep.
InterPro; IPR008030; Grow fac recep.
InterPro; IPR008030; Grow fac recep.
InterPro; IPR008020; Protease S8B.
InterPro; IPR008020; Protease Inhib.
Pfam; PP00082; Peptidase S8; 1.
Pfam; PP000082; Peptidase S8; 1.
ProDom; PD000717; P_domain; 1.
ProDom; PD000717; P_domain; 1.
PROSITE; P800136; SUBTILASE ASP; PALSE_NEG.
PROSITE; P800139; SUBTILASE IIS; 1.
PROSITE; P800139; SUBTILASE SRR; 1.
                          PRT; 1696 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9NJ15-1; Sequence=Displayed;
                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS A; B AND C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF184615; AAF26300.1; -. EMBL; AF184616; AAF26301.1; -. EMBL; AF184617; AAF26302.1; -. HSSP; 099405; 1MPT.
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                 NCBI_TaxID=7738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=B;
                          PCK5 BRACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=C,
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15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1328 LHHGDCDSCHRECKTCDGPHHDNCLSCQPGSYLNDQQCSTHCPRGTPRETYEDDSGBTVL 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1504 Y--NCLSCPYGSKLGBGVCYPMCEBHEYYVBKTQICBECDNSCKTC---RG--STAHDCL 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 DCDFCF--NKNFCFKCKSGFYLHLGKCLDSCPEGL--------EANN 137
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                                                                                                                                                                                                                                                                                                                                                DDTCTACNDGFL/IDASSCEAGCP -> ARKQNQASFCPFA
REWSVILABIALAGHHRYSLIDVPPQSNSPPDTVLGADRARL
TTATSAAGRCA (in isoform C).
/FIId=VSP_005442.
                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (In isoform C).
Tylid=VSP 005442
CHPTIG=VSP 005442
CHPTIGECSDEAGCPEGOFL
HHGDCDSCHRECKTC -> IARCVDRRDRSWCDLVLRENPC
                                                                                                                                                                                                                                                                                                                         DDTILDRGECITSCGPGBYMDRREKKCKACHPTCKBCSDBY
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                   PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                           CLEANAGE (AUTO-) (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENITAL).
N-LINKED (GLCNAC...) (POTENITAL).
N-LINKED (GLCNAC...) (POTENITAL).
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P29122; Q15099; Q15100; Q9URG7; Q9URJ1; Q9URJ2; Q9URJ7; Q9URJ9; Q9VR4G9; Q9Y4G9; Q9Y4H1; Q9URG29; Q9Y4G9; Q9Y4H1; Q1-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 15-MR-2004 (Rel. 44), Last annotation update) 15-MR-2004 (Rel. 45), Last canceation update) (SC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 181.5; DB 1; Length 1696; 23.9%; Pred. No. 2.6e-05; Live 23; Mismatches 72; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 QHPSAKG---KGNLC-----PPTSE-----TRTCIVQRK 206
                                                                                                                                                    CYS-RICH MOTIF (CRM) REGION.
CLEAVAGE (AUTO-) (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1696 AA; 188410 MW; 281CBE1784257CBD CRC64;
                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (In isoform A). /FTId=VSP_005445.
                                                                                           CYTOPLASMIC (POTENTIAL)
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                                                                                                                        CATALYTIC.
  POTENTIAL
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                                                             1618
1639
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1696
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192
233
246
529
885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                           DOMAIN
TRANSMEM
DOMAIN
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PAC4_HUMAN
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Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), Kexin-like processing endoprotease."; J. Biochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Endoprocease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Blochem. J. 339:639-647(1999).
                                                                  Identification of a second human subtilisin-like protease gene in the fes/fps region of chromosome 15.";
NA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K., Tsuji A., Matsuda Y.; "Biosynthetic processing and quaternary interactions of proprotein convertase SPC4 (PACB4).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; PACE4A-II; PACE4CS; PACE4D; PACE4E-I AND PACE4E-II).
MEDLINE=98021085; Pubmed=9378725;
                                                                                                                                                                                                                                                                                 "Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                 'Identification of novel cDNAs encoding human kexin-like protease
                                                                                                                                                      Fsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.,
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                                                                                                                                                                                                                                                                                                                                            TISSUB=Placenta;
Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Cerebellum;
MEDLINE-97335942; PubMed=9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
"A novel human PACE4 isoform, PACE48 is an active processing procontaining a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                      TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; PubMed=1741956;
Kiefer M.C., Tucker J.B., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G., "Functional analysis of human PACB4-A and PACB4-C isoforms identification of a new PACB4-CS isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a novel PACB4 isoform, PACB4B.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 204:1381-1382(1994)
            FROM N.A. (ISOPORMS PACE4A-I AND PACE4B)
                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 200:943-950(1994)
                                                                                                                      FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING (ISOFORM PACE4CS).
MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PubMed=10215603;
                                                                                                                                               MEDLINE=94235049; PubMéd=8179631;
                                                                                                                                                                                                                                             MEDLINE=95071480; PubMed=7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98408849; PubMed=9738469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 396:31-36(1996)
                                                                                                                                                                                               PACE4 isoforms.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99233559
                                                                                                                                 TISSUE=Placenta;
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            SEQUENCE
                                                                                                                     SEQUENCE
                                                                                                                                                                      Matsuda
                                                                                                                                                                                                                                  BRRATUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=29122-8; Sequence=VSP_005436, VSP_005437;
TISSUS SPECIFICITY: Bach PACE4 isoform exhibits a unique restricted distribution. PACE4A-1 is expressed in heart, brain, placenta, lung, skeletal muscle, kidney, pancreas, but at comparatively higher levels in the liver. PACE4A-II is at least expressed in placenta. PACE4B was only found in the embryonic kidney cell line from which it was isolated. PACE4C and PACE4D are expressed in placenta. PACE4E-I is expressed in cerebellum, placenta and pituitary. PACE4E-II is at least present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P29122-6; Sequence=VSP_005427, VSP_005434, VSP_005435; Note=Probably enzymatically Inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PACB4A-II;
ISOId=P29122-2; Sequence=VSP_005436;
Name=PACB4B; Synonyme=PACB4.1;
ISOId=P29122-3; Sequence=VSP_005428, VSP_005429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P29122-4; Sequence=VSP_005432, VSP_005433;
Note=Probably enzymatically inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSP_005431;
                                                                                                                                                                                                                                                                                                                                                                                                     Bvent=Alternative splicing; Named isoforms=8;
Name=PACE4A-1; Synonyms=PACE4;
IsoId=P29122-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=Probably enzymatically inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=P29122-5; Sequence=VSP 005430, Note=Probably enzymatically Inactive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PACE4B-1;
IsoId=P29122-7; Sequence=VSP_005437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
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AB001898; BAA21620.1; JOINED.
AB001900; BAA21620.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=PACE4E-II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB001904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=PACE4C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB001901;
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EMBL;
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Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U., Rentrop M., Gateff B.A.F., Leunissen J.A.M., van de Ven W.J.M.; "Cloning and functional expression of Dfurin2, a subtilisin-like proprotein processing enzyme of Drosophila melanogaster with multiple repeats of a cysteline motif."; J. Blol. Chem. 267:17208-17215(1992).
                                                                                                                                                               Rochrock A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L., van de Ven W.J.M.;

"The Diuz gene of Drosophila melanogaster: genetic organization,

"The Diuz gene of Drosophila and pro-protein processing activity of its translational product Dfuring.";
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                     SEQUENCE FROM N.A.
STRAIN=Oregon-R, Tuebingen, and 180-1;
MEDLINE=92381036; PubMed=151259;
                                                                                                                                                                                                                                            STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                        MEDLINE=95186060; PubMed=7880443;
                                                                                                                                                                                                                 DNA Cell Biol. 14:223-234(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     respective precursors.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                STRAIN=ISO-1;
   206
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P10432, Q24301;
P10-372, Q24301;
P10-382, PEB-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Purin-like procease 2 precursor (RC 3.4.21.75) (Furin 2).
FURZ OR CG18734/CG4235.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 179; DB 1; Length 969; 23.3%; Pred. No. 2.3e-05;
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RA MEDLINE-2019-800-6; PubMed-10731132;

RA Agamer M. D., Celniker S. B., Holt R. A., Fvans C. A., Gocayne J.D.,

RA Agamerides P. G., Scherer S. B., Holt R. A., Hotherton S. N.,

RA Agamerides P. G., Scherer S. B., Holt R. A., Hotherton S. N.,

RA Agamerides P. G., Scherer S. B., Holt R. A., Hotherton S. N.,

Ballaw R. M., Lewis S. B., Richards S., Ashburner M., Henderson S. N.,

Brandon R. C., Rogers Y. H. C., Blazej R. G., Champe M., Pfelffer B. D.,

RA Abril J. P., Agabayari A., An H. J., Andrews-Farankoch C., Baldwin D.,

Ra Ballew R. M., Basu A., Barendale J., Bayraktaroglu L., Beaaley B. M.,

Ballew R. M., Basu A., Bauler H., Galdew E., Center A., Chandra I.,

Ra Burris K. C., Buamen D. A., Buller H., Galdew E., Center A., Chandra I.,

RA Burris K. C., Buamen D. A., Buller H., Galdew E., Center A., Chandra I.,

RA Burris K. C., Buamen D. A., Buller H., Galdew E., Center A., Chandra I.,

RA Burris K. C., Buamen D. A., Buller H., Gar S., Center A., Chandra I.,

RA Glock A., Gong F., Gorrell J. H., Gu Z., Gana P., Harris M.,

Bothon K., Dowy L. B., Downes M., Perriac S., Pleischmann R.,

RA Harris N. L., Harvey D.A., Hamman T. J., Harnede J. R., Houck J.,

RA Harris N. L., Harvey D.A., Hamman T. J., Harnede J. R., Houck J.,

RA Harris M. M. Harban R. S., Howland T. J., Hernanded J. R., Houck J.,

RA Harris M. M. Laker B., McInnosh I. C., Karvitz S., Kulp D., Lai Z.,

RA Harris M., Malson K., Sannders R., North M., Nosherfi A.,

Ramel B. E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Harris M., Malson K., Shanders R.D. C., Scheeler P., Shen H.,

Rainer K., Remington K., Sannders R.D. C., Scheeler P., Shen H.,

Rainer K., Remington K., Sannders R.D. C., Scheeler P., Shen H.,

Spier B., Spradling A.C., Sumper R., Wasser M., Massarman D.A., Nixon K., Nusskern D., Purris R., Marsarman D.A., Nixon K., Nusskern D., Farrog S., Yan S., Bull R.,

Rainer R., Perrid K., Sannders R., Wassarman D.A., Weiner K., Shen S., Marsarman D.A., Nainer R., Wassarman D.A., Nainer R., Wassarman D.A., Nainer R., Wassarma
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us-09-894-912a-32.rsp

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                     nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
TISSUE SPECIFICITY: Transient expression in a subset of central
                                                                              DEVELOPMENTAL STAGE: Expressed both maternally and zygotically. SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
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Multigene family; Zymogen; Repeat.
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GO; GO: 0004276; F.furin activity; IDA.
INTERPO: JRR005212; Furin repeat.
INTERPO: JRR005212; Furin repeat.
INTERPO: JRR005009; PEDTIGASE_SB.
INTERPO: JRR005009; PEDTIGASE_SB.
INTERPO: JRR005084; PEDTIGASE_SB.
INTERPO: JRR009209; PEDTIGASE_SB.
INTERPO: JRR009209; PEDTIGASE_SB.
PROMOSTIE; PROFOTO: PEDTIGASE_SB.
PROMOTIS; PROFOTO: PEDTIGASE_SB.
PROSTIE; PS00134; SUBTILASE_ASP; 1.
PROSTIE; PS00134; SUBTILASE_ASP; 1.
PROSTIE; PS00134; SUBTILASE_BSP; 1.
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EMBL; L33831; AAA69860.1; --
EMBL; AE003502; AAF48598.1; --
PIR; A43434; A43434.
HSSP; Q99405; 1MPT.
MEROPS; S08.049; --
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                                                                  23 NASRGRRORRMHPN---VSQGCQGGCATCSDY--NGCLSCKPRLFFVLERIGMKQIGVCL
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01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(rPC5) (PC6) (Fragment).
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                                 Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE=9314205; PubMed=8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
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De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                 72;
Query Match 11.3%; Score 174; DB 1; Length 1679; Best Local Similarity 24.5%; Pred. No. 8.6e-05; Matches 48; Conservative 15; Mismatches 61; Indels 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
SUBCELULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kydney primordia.
DOMAIN: The propeptide domain acts as an intramolecular chaperone
assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOWAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PAGS-1.
-!- SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
PROPROTBIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMES, PROMOTAS, SUBTILLISIN.
PRINTS; PRO0723; SUBTILLISIN.
PRODOM; PD000717; P_domain; 1.
PRODOM; PD000717; P_domain; 1.
PROSITE; PS00137; SUBTILASE ASP; 1.
PROSITE; PS00139; SUBTILASE HIS; 1.
PROSITE; PS00139; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Cleavage on pair of basic residuee; Alternative splicing; Repeat; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYS-RICH MOTIF (CRM) REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
CATALYTIC.
HOWO B.
                                                                                                                                  Svent=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006212; Purin repeat.
InterPro; IPR000209; Peptidase S8.
InterPro; IPR00284; Peptidase S8B.
InterPro; IPR009020; Protease Inhib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 114933; AAA99906.1; -. EMBL; U47014; AAA87888.1; -.
                                                                                                                  ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
116
1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1768
1789
1877
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602
1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B48225; B48225.
HSSP; Q99405; 1MPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S08.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
1769
1790
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TRANSMEM
DOMAIN
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DOMAIN
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         683 ADKKRCRKCAPNCESCFGSHADQCLSCKYGYPINEFISSCVAQCPEGSYQDIKKNIC--- 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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Thacker C., Srayko M., Rose A.M.;
*Mutational analysis of bli-4/kpc-4 reveals critical residues required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLPPVLERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR------ICVSSCPPGHP---H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cuticle protein 4).
BLI-4 OR KPC-4 OR KO4F10.4.
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                 ATERSWARGGFCMLVKKNINLCQRKVLQQLCCKTCTPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLI4_CAREL STANDARD; PRT; 943 AA.
P51559; 044762; 044764; 044765; 044766;
01-007-1996 (Rel. 34, Created)
10-007-2003 (Rel. 41, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Bndoprotease bli4 precursor (BC 3.4.21.-) (Blisterase) (Blistered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 VHCRASEWSPWSPCMKKGKTC-GPKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GKCSENCKTCTGPHNCTECKGGLSLQ------GSRCSVTCB 774
                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
                                           (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thacker C., Peters K.W., Srayko M., Rose A.W., athe bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/subtilisin-like endoproteases essential for early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 164; DB 1; Length 1877; 27.7%; Pred. No. 0.00047; tive 20; Mismatches 57; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND FUNCTION.
STRAIN-Bristol N2;
MEDLINE-95293228; PubMed=7774813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform PC5A). /PTId=VSP_005441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Latreille P., Wamsley P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                        CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CLEAVAGE (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                       (in isoform PC5A) / PTId=VSP 005440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development and adult morphology." Genes Dev. 9:956-971(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1877 AA; 207888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 27.7
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
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                                                ACT_SITE
ACT_SITE
ACT_SITE
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CARBOHYD
CARBOHYD
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CARBOHYD
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Matches
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    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        ISOIG=P51559-5; Sequence=VSP 005417, VSP 005420;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
TISSUB SPECIFICITY: In larvae and adults, expressed in all
hypodermal cells, vulva and ventral nerve cords.
DBVELOPMENTAL STAGE: Expression starts at embryo two-fold stage
through to adults.
SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in postion 651.
CAUTION: Ref.2 (AAB96754 and AAB96757) sequence differs from that
shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormDep; NG4F10.45; CB11728.

R WormDep; RG4F10.44; CB11730.

R WormDep; RG4F10.44; CB11731.

R WormDep; RG4F10.44; CB11732.

R WormDep; RG4F10.44; CB11732.

R G0: 00.010.021; C:integral to membrane; NAS.

R G0: 00.010.21; C:integral to membrane; NAS.

R G0: 00.010.22; F:serine-type endopeptidase activity; NAS.

G0: G0:0007592; P:cuticle biosynthesis (sensu Invertebrata); IMP.

R InterPro; IPR00201; Purin repeat.

R InterPro; IPR00209; Poptidase SB.

InterPro; IPR00209; Peptidase SB.

InterPro; IPR00900; Protease Inhib.

R Pfam; PP00183; P_proprotein; I.

R Pfam; PP00183; P_proprotein; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Calcium-binding; Zymogen; Transmembrane; Signal; Alternative splicing.
for proprotein convertase function in C. elegans.";
Gene 252:15-25(2000).
-!- FUNCTION: The Kex2/subtilisin-like proteinase activity of this enzyme is required for the normal production of adult cuticle.
There is functional redundancy between the isoforms. Vital for embryonic and larval development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENDOPROTEASE BLI-4.
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                   Name=A; Synonyms=a;
IsoId=P51559-2; Sequence=VSP_005416, VSP_005419;
Name=B; Synonyms=b;
IsoId=P51559-3; Sequence=VSP_005418, VSP_005421;
Name=C; Synonyms=c;
IsoId=P51559-4; Sequence=VSP_005422, VSP_005423;
                                                                                                           Bvent=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                        IsoId=P51559-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L29438; AAA98750.1; ALT_FRAME.
EMBL; L29449; AAA98751.1; ALT_FRAME.
EMBL; AF039719; AAB96753.1; -L.
EMBL; AF039719; AAB96753.1; -L.
EMBL; AF039719; AAB96755.1; -L.
EMBL; AF039719; AAB96755.1; -L.
EMBL; AF039719; AAB96755.1; -L.
EMBL; AF039719; AAB96756.1; -L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P domain; 1.
SMART; SM00261; PU; 3.
                                                                                                                           Name=D; Synonyms=d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 YYGTRYPDINKCTKCKVDCDTCPNKNPCTKCKSGFYL-----HL--GKCLDSCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 ADYES----NLVQAK------CIWRKDLCGDG-----YYINAVGKCDLCDS 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ANNHIMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTBTRVRDILQHPSAKGKGNLCPP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         828 // CONTRACTOR CONT
                                                                                                                                                                                                                                          180form A)
VERANSSPPDLTSGWKLSCDECNGGCTESSSATSCFAYKH
V -> LCFNFENSOPTECVCLRVCEPGVIINFQIEKLKKST
                                                                                                                                                                                                                                                                                                                                                                                                                                             VEESARSSFPDLTSGWKLSCDECNGGCTESSSATSCFAYKH
TYTLANGSGSFKVCHOOTYTLDGDKCKM -> GDEVV
ERIRNHWEVTLEESSHWIWELARBHKSLOELANSSSETHSPL
YSFTKFQPIPLILVCIPDAIHRQFAV (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 RRMHPNVSQG------CQGGCATCSDYNGCLSCKPRLFFVLBRIGMKQIGVCLSSCPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 RSSFPDLTSGWKLSCDECNGGCTESSSATSCPAYK-HLTQTLRNKGGSGF-KCVQKCDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein PACE4.
(BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                          VBESARSSPPDLT -> ILITIAIHLVVNA (in
                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 10.6%; Score 162; DB 1; Length 943; Best Local Similarity 27.1%; Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform A).
/FTId=VSP 005419.
Missing (In isoform E).
/FTId=VSP 005420.
                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform B) / Frid=VSP_005421.
                                                                                                                                                                                                                                                                                                                                                                          KCLIFS (in isoform E).
       CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP 005418
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         937 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 TSETRIC--IVQRICKSKG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813 SCETCTAPGPMSCEKCSKG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Conservative
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       241
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346 3
943 AA;
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Q63415;
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         WEDLINE=9449873; PubMed=8070361;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
Juliary and regulated by thyroid status.";

Ridocrinology 135:1178-1185(1994).

-! FUNCTION: Likely to represent an endoprotease activity within the constitutive secretory pathway, with unique restricted distribution in both neuroendocrine and non-neuroendocrine tissues and capable of cleavage at the RKIK/RNR consensus motif.

-! CATALTITE ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.
                                                                                                                                                                                                                                               COPACTOR: Calcium (Potential).
TISSUE SPECIFICITY: High expression in the anterior pituitary and in several brain regions, the atrium, and the ventricle.
DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAIRED BASIC AMINO ACID CLEAVING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SWUUZE; :.,
PROSITE; PSS0900; PLAC; 1.
PROSITE; PS00137; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
HYdrolase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium; Cleavage on pair of basic residues; Repeat.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (FOTENTIAL).
N-LINKED (GLCNAC. . ) (FOTENTIAL).
N-LINKED (GLCNAC. . ) (FOTENTIAL).
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STRAIN-Sprague-Dawley; TISSUE-Hypothalamus, and Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYS-RICH MOTIF (CRM) REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104053 MW; F3865557C33705C8 CRC64;
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CELL ATTACHMENT SITE
                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to peptidase family $8. -!- SIMILARITY: Contains 1 homo B/P domain. -!- SIMILARITY: Contains 1 PLAC domain.
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InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR0020920; Protease_Inhib.
Pfam; PP01483; P_proprotein; I.
Pfam; PP00082; Peptidase_S8; I.
PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L31894; AAA61987.1; -. PIR; I53282;
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MEROPS; S08.075; -.
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CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NFCTKCKSGFYLHLGKCLDSCPEGLE 134
                                                                           135 ANNHTMEC-----PWSTVHCEAS----EWS------PWSP 158
                                                                                                            806 PDSELIRCGECHHTCRICVGPSREBCIHCAKSFHFODWKCVPACGEGFYPREMPGLPHKV 865
                                                                                                                                                    159 CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRTCIVQRK 206
                                                                                                                                                                                     866 CRRCDENCISCEGSSRNCSRCKAGFIQIGTSCITNHTCSNADETFCEMVKSNRLC--ERK 923
                       Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-) (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=092824-1, Sequence=Displayed; TISSUE SPECIFICITY: Expressed in T-lymphocytes. DOMAIN: The propertide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=6635380; PubMed=8755538; Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; Isolation of the human PCG gene encoding the putative host protease for HIV-1 gpl60 processing in CD4+ T lymphocytes."; Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Franzusoff A., Miranda L., Wolf J., Pichuantes S., Lu Y., Duke Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reudelhuber T.L.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bvent=Alternative splicing; Named isoforms=1;
Comment=2 isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to peptidase family S8. SIMILARITY: Contains 1 homo B/P domain. SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                                                                                                                                      Q92874; Q13527;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                      913 AA
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10.5%; Score 161; DB 1; Length 937; 22.5%; Pred. No. 0.0004;

12;

72; Gaps

90; Indels

24; Mismatches

54; Conservative

Local Similarity

Best Loca Matches

Query Match

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activities."
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93 NKCTKCKVDCDTCENK--NPCTKCKSGFYLH--LGKCLDSCPEGLEANNHTMECVSIVHC 148 : | | | : | : | | | | | | | | | | |
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                                                                                      MIM, 600488; -..

MIM, 600488; -..

MIM, 600488; -..

GO; GO:0005252; P:serine-type endopeptidase activity; TAS.

GO; GO:0005252; P:serine-type endopeptidase activity; TAS.

GO; GO:0005252; P:serine-type endopeptidase activity; TAS.

MICHERPO: IPRO00219; P:protectory and peptidolysis; TAS.

InterPro: IPR000219; P:protectors and peptidols 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 EASEWSPWSPCMKKGKTC-GPKRGTETRVRDILQHPSAKGKGNLCPPTSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 154; DB 1; Length 913; 28.2%; Pred. No. 0.0012; tive 23; Mismatches 57; Indels 4
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CYS-RICH MOTIF (CRM) REGION.
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or send an email to license@isb-sib.ch)
                 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINES-9221557; PubMed=10201374;
MEDLINES-9221557; PubMed=10.3174;
Misch J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;
"A new secreted protein that binds to Wnt proteins and inhibits their
                                                                                                            Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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WMT INHIBITORY FACTOR 1.
WIF.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
WNT inhibitory factor 1 precursor (WIF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGP-LIKE 1.
EGP-LIKE 2.
EGP-LIKE 4.
EGP-LIKE 4.
EGP-LIKE 4.
EGP-LIKE 5.
EGP-LIKE 5.
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EGP-LIKE 1.
EGF-LIKE 6.
EGF-LIKE 6.
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InterPro; IRR006209; EGF like.
InterPro; IRR006209; EGF like.
InterPro; IRR002049; Laminin_EGF.
InterPro; IRR003040; WIF.
InterPro; IRR03306; WIF.
Ffam; PP000069; EGF; S.
Ffam; PP000069; EGF; S.
Ffam; PP00019; EGF; S.
FRART; SM00469; WIF; 1.
PROSITE; PS00022; EGF 1; S.
PROSITE; PS01186; EGF 2; S.
PROSITE; PS50184; WIF; 1.
PROSITE; PS50184; WIF; 1.
PROSITE; PS50184; WIF; 1.
PROSITE; PS50184; WIF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 BCVSIVHCEASEWSPWSPCMKKGKTCGPKRGTETRVRDILQHPSAKG-KGNLC----P 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 PISBIRICIVQRK-KCSKGERGKKGRERKRKKLNKEERKETSSSSDSKGLESSIETPDQQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCRNGGFCNDRHVCECPDGFYGPHCEKALCMPRCM-----NGGLCVTPGLCIC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 SCGAHGTCIBPNKCQCKEGWNG-----RYCNKKYGSNLMNALRPTGSRNRQHTPSPK 359
                                                                                                                                                                                                                                                                                                                                                                              41 COGGCAT---CSDYNGC-----LSCKPRLFFVLERIGMKQIGVC---LSSC 80
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-!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH APPINITY AND IGF II WITH A LOWER APPINITY. IT HAS A
                                                                                                                                                                                                                                                                                                                   78; Indela 85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QCRTSKCQ--QPCRNGGKCSGKNK------CKCSKGYQGDLCSKPVCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Du J., Delafontaine P.;
"Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leroith D.; \label{eq:control} \mbox{"Developmental regulation of the rat insulin-like growth factor I}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                                                                        923 POTENTIAL.

83 N-LINKED (GLCNAC. . . ) (POTENTIAL)

240 N-LINKED (GLCNAC. . . ) (FOTENTIAL)

41071 MM; RZ6F973B0F00ACFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FSB-2003 (Rel. 41, Last amnotation update)
Insulin-like growth factor I receptor precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                  10.0%; Score 153.5; DB 1; Length 374; 24.4%; Pred. No. 0.00056;
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MEDLINE-92412145; PubMed=1530648;
Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
"A new member of the insulin receptor family, insulin
receptor related receptor, is expressed preferentially in the kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
                                                                                                                                                                                                                                                                                                                   23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1370 AA.
                             POTENTIAL.
POTENTIAL.
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MEDLINE=90017496; PubMed=2477843;
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                                                                                                                                                                                                                                                                                                                   60; Conservative
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374 AA;
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                             DISULPID
                                                                                           DISULPID
CARBOHYD
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                                                                                                                                                             CARBOHYD
                                                                                                                                                                                       SEQUENCE
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                                    tyrosine phosphate.
SUBGINIT: TETRAMEN OP 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOWAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOWAIN. SUBCELLULAR LOCATION: Type I membrane protein.
SUBCRILULAR LOCATION: Type I membrane protein.
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(POTENTIAL).
(POTENTIAL).
TYROSINE-PROTEIN KINASB ACTIVITY.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                    -!- SIMILARITY: Contains 2 fibronectin type III domains
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PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
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N-LINKED (GLCNAC...
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ATP (BY SIMILARITY)
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EMBL; M27293; AAA41384.1; -.
HSSP; P06213; IIRK.
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                                                                                                                                                                                                                                                                                                                                                                                                                        94 KCTKCKVDCDTCFN-KNFCTKCKSGFYLHLGKCLDSCPEGLEANN-HTMECVSIVHCEAS 151
                                                                                                                                                                                                                                                                                                                                      34 HPNVSQGCQGGCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo;

MEDLINE=93176785; PubMed=8367492;

Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;

Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;

"Ectopic neural expression of a floor plate marker in frog embryos injected with the middline transcription factor Pintallavis.";

Proc. Natl. Acad. Sci. U.S., 90:8568-8272(1993).

-!- FUNCTION: Promotes the attachment of spinal cord and sensory neuron cells and the outgrowth of neurites in vitro. May contribute to the growth and guidance of axons in both the spinal cord and the PNS.
                                                                                                                                                                                                                                                                                                       57; Indels 40; Gaps
                                                                                                                                                                                                         66 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
86 AD -> PY (IN RBF. 3).
155395 MM; A5946897A41CB145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed at high levels in the floor plate.
-!- SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-spondin precursor.
Ranopus lavis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                            (POTENTIAL)
                                                                                                                                                                                                                                                                     9.7%; Score 149; DB 1; Length 1370; 28.7%; Pred. No. 0.0039; tive 20; Mismatches 57; Indele 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 EWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKG----KGNL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GPC---PKVCGDERKKTKTIDSVTSAQMLQGCTILKGNL 361
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
N-LINKED
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                       1370 AA;
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CARBOHYD
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EMBL; L09123; AAA19105.1; -.

PIR; A47723; A47723

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144 SIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKGKGNLCPPTSETRTCIV 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 606 TIPCVLSPWSEWSDCSVTCGKGTRTRQR----MLKSPSBLGDCNBELBLKQVBKCMLPBCP
                                                                                                                                                                                                                                                                                                                                                     57 CKPRLFFVLB------RIGMKQIGVCLSSCPSGYYGTR-YPDINKCTKCKV---
                                                                                                                                                                                                                                                                                                                                                                                                                    101 -----DCDTCFNKORFCTKCKSGFYLHLGKCLDSCPEGLEANN----HTMBCV
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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-!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jaggedl, Jagged2 and Deltal to requlate cell-fate determination.
Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21331789; PubMed=11438922;
Irvin D.K., Zurcher S.D., Maynen T., Weinmaster G., Kornblum H.I.;
Expression patterns of Notchl, Notch2, and Notch3 suggest multiple
functional roles for the Notch-DSL signaling system during brain
                                                                                                 P.SPONDIN.
TSP TYPE-1 1.
TSP TYPE-1 3.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 6.
N-LINERD (GLCNAC. . .) (POTENTIAL).
N.LINERD (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                          DB 1; Length 803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QWJ0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2)
NOTCH2.
                                                                                                                                                                                                                                                                                          9.5%; Score 145.5; DB 1; Length 26.6%; Pred. No. 0.0041; ive 23; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 ORKKCSKGERGKKGRERKRKKLINKEERKETSSSSDSKG 241
                                                                                        Cell adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Brain;
MEDLINE-91202015; PubMed=1295745;
MeDLINE-91202015; PubMed=1295745;
Whotch2: a second mammalian Notch gene.";
Development 116:931-941(1992).
                         Pfam; PF02014; Reeler; 1.
Pfam; PF00090; tsp 1; 6.
SMART; SM02209; TSP1; 6.
PROSITE; PS50092; TSP1; 6.
Glycoprotein; Signal; Repea
                                                                                                                                                                                                                                                               90702
                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                               803 AA;
                                                                                                                                                                                                                                                                                                          Local Similarity
Hes 58; Conserv
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us-09-894-912a-32.rsp

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NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.
NOTCH EXTRACELLULAR TRUNCATION (BY
SIMILARITY).
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H HSSP; P00743; 1CCF.

R HSSP; P00743; 1CCF.

R InterPro; IPR0001210; AMK.

R InterPro; IPR0001210; AMK.

R InterPro; IPR0001881; EGF_Ca.

R InterPro; IPR001881; EGF_Ca.

R InterPro; IPR001881; EGF_Ti.

R InterPro; IPR001809; EGF_Ti.

R InterPro; IPR002049; LamInin_EGP.

R InterPro; IPR002049; LamInin_EGP.

R InterPro; IPR002049; LamInin_EGP.

R InterPro; IPR002050; Motch_dom.

R Fdam; PP00066; Motch, 2.

R Fdam; PP00066; Motch; 3.5.

R Ffam; PR00010; EGFBLOOD.

R PRINTS; PR00011; EGFLAMININ.

R RINTS; PR00011; EGFLAMININ.

R SWART; SW00014; EGF_CA; 24.

SWART; SW00014; MI; 2.

R R SWART; SW000248; AMK REP REGION; 1.

R R PROSITE; PS50018; AMK REPERED;

R R PROSITE; PS50002; EGF_2; 24.

R R PROSITE; PS50018; EGF_2; 25.

R R PROSITE; PS01187; EGF_CA; 22.

R R PROSITE; PS01187; EGF_CA; 22.

R R PROSITE; PS01187; EGF_CA; 24.

R R PROSITE; PS01187; EGF_CA; 22.

R R PROSITE; PS01187; EGF_CA; 22.

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R R PROSITE; PS01187; EGF_CA; 22.

R R PROSITE; PS01187; EGF_CA; 22.

R R PROSITE; PS01187; EGF_CA; 24.

R PROSITE; PS01187; EGF_CA; 24.

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R PROSITE; PS01187; EGF_CA; 24.

R PROSITE; PS01187; EGF_CA; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 SAKGKGNLCPPTSETRTCIVQRKKCSKGE-----RGKKGRERKRKKLNKEE---- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 LDSCPEGLEANNHTM--ECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHP 183
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TSP TYRE-1 1.
TSP TYRE-1 2.
TSP TYRE-1 3.
TSP TYRE-1 4.
TSP TYRE-1 6.
TSP TYRE-1 6.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGIR MOUSE STANDARD; PRT; 1373 AA.

Q60751; 070438; Q62123;
061-NOY-1997 (Rel. 35, Created)
11-007-2001 (Rel. 40, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor I receptor precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.1%; Score 142.5; DB 1; Length 807; Best Local Similarity 29.5%; Pred. No. 0.0066; Matches 54; Conservative 16; Mismatches 60; Indels 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE PROM N.A.
Navarro M., Garandel V., Barenton B., Bernardi H.;
"Cloning of cDNA for the mouse insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                          Cell adhesion.
                                                                                                                                                                EMBL; M88469; AAA41174.1; -...
PIR; A38152; A38152.
InterPro; IPR002861; Reeler.
InterPro; IPR002864; TSP1.
Pfam; PP02014; Reeler; 1.
Pfam; PP0090; tsp 1; 6.
SWART; SM0209; TSP1; 6.
PROSITE; PS50092; TSP1; 6.
Glycoprotein; Signal; Repeat; CS SIGNAL.
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SEQUENCE OF 1-329 FROM N.A.
STRAIN=CD-1; TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 P-DINKCTKCKVDCDTCFNKNFC------TKCKSGFYLHLGK 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 ORRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurite extension.";
Cell 69:95-110(1992).
-!- FUNCTION: Promotes the attachment of spinal cord and sensory
neuron cells and the outgrowth of neurites in vitro. May
contribute to the growth and quidance of axons in both the spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Gaps
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Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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SUBCELLULAR LOCATION: Secreted.
TISSUR SPECIFICITY: Expressed at high levels in the floor plate.
SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-Embryonic floor plate;
MEDLINE-92208952; PubMed-1555244;
Klar A., Baldassare M., Jessell T.M.;
"F-spondin: a gene expressed at high levels in the floor plate encodes a secreted protein that promotes neural cell adhesion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 144.5; DB 1; Length 2471;
; Pred. No. 0.014;
25; Mismatches 54; Indels 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RPRC----LCPPGWDGAYCDVLNVSC-KAAALQKG 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Last sequence update) 28-PBB-2003 (Rel. 41, Last annotation update)
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01-JUN-1994 (Rel. 29, Created)
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STRAIN=C57BL/6; TISSUE=Thymus;
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                                                         MEDIANE OF 1134-1203 FROM N.A.

MEDIANE-90152381; Pubbed-2482828;

WILLAR A.F., Kurban R.R., Hovens C.M., Ralph S.J.;

WILLAR A.F., Kurban R.R., Hovens Chain reaction to cloning members of the protein tyrosine kinase family.";

of the protein tyrosine kinase family.";

C.I. PUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)

TYROSINE-FROTENIX TANASE ACTIVITY.

C.I. CHALYTIC ACTIVITY: AND IGF II WITH A LOWER AFFINITY. IT HAS A TROSINE PROPERING FOR THE PROPERING CO.T. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

C. SUBUNITY: TETRARREN OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULPIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOWAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOWAIN.

C. SUBCELLULAR LOCATION: Type I membrane protein.

C. SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
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Jun W., Liu Z., Alvares K., Kumar A., Wallner B.I., Kanwar Y.S., Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
SIGNAL 31 741 INSHIAN-LITER CENTER ENTER OF THE CHAIN
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRR00391; FN_III.
InterPro; IRR005211; Furin-like.
InterPro; IRR005212; Furin-like.
InterPro; IRR009030; Grow Fac recep.
InterPro; IRR000719; Prot kinase.
InterPro; IRR002011; ReceptrykinsII.
InterPro; IRR001245; Tyr_pkinase_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD, MGI:96433, Igfir.
GO:00099887; Prorganogenesis; IMP.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR0008957; FW_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP056187; AAC12782.1; --
EMBL; U00182; AAC52123.1; --
EMBL; M3422; AAA40013.1; --
PIR; A48805; A48805.
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94 KCTKCKVDCDTCFN-KNPCTKCKSGFYLHLGKCLDSCPEGLBANN-HTMECVSIVHCBAS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 HPNVSQGCQGCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYC2 MOUSE STANDARD; PRT; 2470 AA.
035516; Q06008; Q60941;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3%; Score 142; DB 1; Length 1373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 EWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKG----KGNL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1145 1145 V -> D (IN RBP. 3).
1202 1202 V -> I (IN RBP. 3).
1373 AA; 155787 MM; 58B3B72BF101B379 CRC64;
                                                                                                                                                                                                                    N-LINKED GLCNAC...)
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C -> S (IN RBF. 2).
D -> G (IN RBF. 2).
B -> V (IN RBF. 2).
C -> S (IN RBF. 2).
V -> I (IN RBF. 3).
V -> D (IN RBF. 3).
V -> I (IN RBF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FL -> LV (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Conservative
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                              DISULPID
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DISULPID
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MEDLINE=1374376; PubMed=11459941;

Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

"Conservation of the biochemical mechanisms of signal transduction
among mammalian Notch family members."

"E among mammalian Notch family members."

"E proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"I proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"I proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"I proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"Open ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.

Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation.

"I submunt: Heterodimer of a Cterminal fragment N(TM) and a N-terminal fragment N(BC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=035516-2; Sequence=VSP_001405; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95333893; PubMed-7609614;
Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.;
"Differential expression of Notchl and Notch2 in developing and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not heart.
DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Muration in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
Development 126:3415-3424(1999).
Hamada Y., Higuchi M., Tsujimoto Y.;
Complete amino acid sequence and mutliform transcripts encoded by
single copy of mouse Notch2 gene.";
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein. Pollowing proteolytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
                                                                                                         SEGUENCE OF 316-1518 FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
MEDLINE=93178563; PubMed=8440332;
Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in wide variety of tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21523956; PubMed=11518718;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                    Martin D.I.; "Inhibition of granulocytic differentiation by mNotchl."; Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R., Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brain Res. Mol. Brain Res. 29:263-272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lsold=035516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteolysis.";
J. Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99396706; PubMed=10393120;
                                                                                                                                                                                                                                                                                      SEQUENCE OF 1765-2153 FROM N.A. MEDLINE=97075110; PubMed=8917536;
                                                                                                                                                                                                                                             Exp. Cell Res. 204:364-372(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse brain.
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the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.

TWIS Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(BC). Following ligand binding, it is cleaved by TNP-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN
NOTCH EXTRACELLULAR TRUNCATION.
NOTCH INTRACELLULAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transcription regulation; Activator; Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P16109; 1PSB.
MGD; MGI:97364; Notch2.
GO; GO:0005887; C:integral to plasma membrane; IC.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0002011; P:morphogenesis of an epithelial sheet; IMP.
GO; GO:0007219; P:N signaling pathway; IC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Developmental protein; Repeat; ANK repeat; BGF-like domain;
Transmembrane; Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                               from the membrane.
--- PTM: Phosphorylated.
--- SIMILARITY: Belongs to the NOTCH family.
--- SIMILARITY: Contains 35 BGP-like domains.
--- SIMILARITY: Contains 2 Lin/Notch repeats.
--- SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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PROSITE, PS50088, ANK_REPEAT; 4.
PROSITE, PS00010, ASK HYDROXYL, 22.
PROSITE, PS00122, EGF_1; 33.
PROSITE, PS01186, RGF 2; 27.
PROSITE, PS50126, RGF 2; 27.
PROSITE, PS50126, RGF 2; 27.
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InterPro; IPR000110; ARK.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR001431; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006409; EGF_II.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR008009; Notch_dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP00023; ank; 6.
Pfam; PP00008; BGF; 34.
Pfam; PP00006; notch; 2.
PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR00011; BGFLAMININ.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D32210; BAA22094.1; -. EMBL; X68279; CAA48340.1; -. EMBL; U31881; AAC52924.1; -. PIR; A49175; A49175.
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SMART; SM00179; EGF CA; 23.
SMART; SM00004; NL; 3.
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(POTENTIAL).				CALCIUM-BINDING	(INCOMPLETE).	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING		CALCIUM-BINDING	_	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING		CALCIUM-BINDING	CALCIUM-BINDING		CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING			CALCIUM-BINDING	CALCIUM-BINDING	CALCIUM-BINDING								DB 1; bength 24/0;	026;
CYTOPLASMIC	EGF-LIKE 2.	EGF-LIKE 3.	EGP-LIKE 4.	'n	EGF-LIKE 6 (BGP-LIKE 7,	EGP-LIKE 8,	EGP-LIKE 9,	EGF-LIKE 10.	EGF-LIKE 11,	EGF-LIKE 12,	EGP-LIKE 13,	EGP-LIKE 14,	EGP-LIKE 15,	EGP-LIKE 16,	BGP-LIKE 17,	BGF-LIKE 18,	EGP-LIKE 19.	EGP-LIKE 20,	BGF-LIKE 21,	BGF-LIKE 22.	EGP-LIKE 23,	EGP-LIKE 24,	EGP-LIKE 25,		EGP-LIKE 27,			EGP-LIKE 30,		EGF-LIKE 32,	EGF-LIKE 33.	BGP-LIKE 34.	EGF-LIKE 35.	LIN/NOTCH 1.	LIN/NOTCH 2.	ANK 1.		score 140.5;	Pred. No. 0.026;
2470	102	143	180	219	256	294	334	372	411	452	490	528	266	603	641	678	716	753	791	829	869	907	945	983	1021	1059	1097	1145	1183	1221	1260	1300	1345	1410	1454	1533	1869	ć		ty 24.4%;
1699	6.49	105	144	182	221	258	296	336	373	413	454	492	530	568	605	643	680	718	755	793	831	871	606	947	985	1023	1061	1099	1147	1185	1223	1262	1302	1372	1418	1501	1825		0.1.1.1	Similari
DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	REPEAT	REPEAT	REPEAT	1000	Query march	Best Local Similarity
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Query Match 9.2%; Score 140.5; DB 1; Length 2470; Best Local Similarity 24.4%; Pred. No. 0.026; Matches 54; Conservative 24; Mismatches 56; Indels 87; Gaps 14;

8 8 8 8

Search completed: June 29, 2004, 17:00:17 Job time : 9.46481 secs Q910k0 mus musculu Q8ayl8 rana escule Q94214 brachydanio Q9u018 giardia lam Q96411 brachydanio Q96p4 homo sapien Q86p4 homo sapien Q86p4 rattus sp. Q9qv4 rattu

mus musculu mus musculu mus musculu Q8k2q8 mus musculu Q8vcc9 mus musculu Q991e4 mus musculu

cryptospori homo sapien

ephydatia f

homo sapien homo sapien caenorhabdi

QBr0y1 r Q23832 cc Q9hcb6 h Q9y1x8 e Q9y1x8 e Q8ncd7 h Q8ncd7 h Q86jw7 l Q86jw7 l Q86jw7 l Q86jw7 l

homo sapien homo sapien

giardia lam giardia lam

17

Perfect score:

Run on:

Sequence:

Scoring table:

Total number

Database

Searched:

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SEQUENCE FROM N.A. May Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S., Mao Y., Xie Y., Zhou Z., Zhao W., Zhao R., Mu C., Tang R., Chen X., Wu C., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Straubberg R.;
Straubberg R.;
Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF2510157; AARX4947.1;
Genew; HGNC:20866; THSD2.1;
InterPro; IPR006212; Furin repeat.
InterPro; IPR009303 Grow Fac_recep.
InterPro; IPR009804; TSPI.
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272 AA; 30928 MW; CACAEC6B7E781189 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                               Q8K2Q8
Q8VCC9
Q8VCC9
Q8DLE4
Q8R0Y1
Q9Y1X8
Q8VCD6
Q8CD7
Q8CD7
Q8CD7
Q8CD7
Q8CD7
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Q91VK0
Q8AY18
Q964D2
O42114
Q9U018
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09QVW4
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Q9PVZ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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913
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Homo sapiens (Human)
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TISSUE=Placenta;
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Q96k87 homo sapien
Q96sb2 mus musculu
Q9cab2 mus musculu
Q9z132 mus musculu
Q9z135 homo sapien
Q9bfu0 mus musculu
Q9ugb2 homo sapien
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                                                                                                                                                                                                                                                                                                                    1 MHLRLISCPFIILNFWEYIG......QKRRARDKQQKSVSVSTVH 279
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           1017041 seqs, 315518202 residues
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Q96K87
Q9CSB2
Q9BWW2
Q9Z132
Q9RN7L5
Q9BW7L5
Q9UGB2
Q9UGB2
Q9UGB2
Q7TPX3
Q8N6X6
Q7TPX3
Q8N6X6
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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Maximum DB seq length: 2000000000
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sp_bacteria:*
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sp_plant: *
sp_rodent: *
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sp_human:*
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110:
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1 MHLRLISCPFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 60

85.7%; Score 1315.5; DB 4; Length 272; 87.1%; Pred. No. 1.8e-110; ive 11; Mismatches 18; Indels 7;

Local Similarity 87.1 hes 243; Conservative

Best Loca Matches

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035171 08CFZ2 Q62030

1315.5 1273 1212 1212 1107 616.5 565.5 565.5 450 449.5 449.5 189.5 183.5

Result

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Query Match

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241 GLESSIETPDOOENKEROOOOKRRARDKOOKSVSVS 276
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                                                                                                       61 LPPALERIGHKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
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                                                                                                                                                                                                  121 HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                      QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKEBRKRTSSSSDSK 240
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1 MHLRLISWLFIILINFWEYIGSQNASRGRRQRRWHPNVSQGRQGRQGGATCSDYNGCLSCKPR
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I Sogai T., Ota T., Hayashi K., Sugiyama T., Oteuki T., Suzuki Y.,

I Isogai T., Ota T., Hayashi K., Sugiyama T., Oteuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugano S., Takahashi-Pujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Nubo human cDkA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO27346; BAB55051.1;

I Submitted (MAY-2001) form Facereep.

R InterPro; IPR000930; Grow Fac_recep.

InterPro; IPR00301; Furin repeat.

InterPro; IPR00301; Furin repeat.

R Pfan; PR00090; tsp.l; 1.

R SMART; SM00261; FU: 2.

SMART; SM00261; TSP1; 1.
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Homo sapiens (Human).

Homo sapiens (Human).
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Hypothetical protein.
SEQUENCE 292 AA; 33243 MW; 01E2774AC3D4A6F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   241 GLESSIETPDQQENKERQQQQKRRARDKQQKSVSVSTVH 279
                                                                                                                                                                                                                                                                                                                                                                                               237 SLESSKEIPEQRENK--QQQKQRKVQDK-QKSVSVSTVH 272
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel.
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RMD; MGJ; MGJ: IPRO00301; Grow Fac_recep.

RICEPPO; IPRO00301; Grow Fac_recep.

RICEPPO; IPRO00303; Grow Fac_recep.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1212; DB 11; Length
Pred. No. 3e-101;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 AA; 24304 MW; ODCF938E9FB3FBF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QHPSAKGKGNLCPPTSETRTCIVQRKKCSKGERGKKGRE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHPSA--KGNLCPPTSETRTCIVQRKKCSKGERGKKGRE 217
                                                                                                                                                                                                                                              OCCSB2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
2810459H04Rik protein (Fragment).
237 SLESSKEIPBQRENK--QQQKKRKVQDKQKSGIEVT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUB=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 79.0%;
al Similarity 98.6%;
216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50092; TSP1; 1.
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SMART; SM00261; FU; 2.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                    PRELIMINARY;
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us-09-894-912a-32.rspt

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InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR0084; TSP1.
SWART; SM00261; EP; 2.
SWART; SM00209; TSP1, 1.
PR0STTE; PS0092; TSP1, 1.
SROUTE: 265 A3; 29331 MW; PFEBB964743F5963 CRC64;
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Interpro; IPR009030; Grow fac_recep.
Interpro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 -----NSRHKGQQQPQ 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS50092; TSP1; 1.
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Matches 112, Conservative
                                                                                                                                                                                                                                                                                              Best Local Similarity 43.7
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00090; tsp 1, 1.
SMART, SM00261, FU; 2.
SMART, SM00209; TSP1, 1.
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                                                                                                                                                                                                                                                                   Query Match
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QBN7L5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LFPVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVDCDTCFNQNPCTKCKSGFYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HILLISCPPIILNPMEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHLRLISCPFIILNFMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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"R-spondin, a novel thrombospondin type 1 domain gene, expressed in
the dorsal neural tube.",
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AB016768; BAA75640.1; --
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.1%; Score 1107; DB 11; Length 224; BB.4%; Pred. No. 8.7e-92; ative 5; Mismatches 19; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHPSAKGKGNLCPPTSBTRTCIVQRKKCSKGBRGKKGRBRKRKK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 OHPSA--KGNPVPPNORDKNLYSTKKEVFKGRARKKGKREKTKK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00261; FU; 2. SEQUENCE 224 AA; 25398 MW; BC13B083497CFEB3 CRC64;
                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow fac recep.
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RSPONDIN OR R-SPONDIN.
                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:2183426; Repondin
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Matches 198; Conservative
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                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                    THSD2 OR 2810459H04RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                Thrombospondin homolog
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Q9Z132;
                                                                                                                                                   Q8BVW2;
                                                                                                                           OBBUW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PFVLERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGFYL 120
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakametsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Ho Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakwa R., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
NECO human cDNA sequencing project.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO98225; BAC02563.1;
                                                                                                                                                                                                                                                                                                                                                                                         3 LRLISCPP-IILNPMBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL
                                                                                                                                                              14; Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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41.2%; Score 632; DB 11; Length 265; 43.7%; Pred. No. 5.8e-49; tive 42; Mismatches 91; Indels 1
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SEQUENCE 236 AA; 25942 MW; 8D03803127EC5678 CRC64;
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01-OCT-2002 (TIEMBLEEL. 22, Last sequence update)
01-OCT-2003 (TIEMBLEEL. 25, Last annotation update)
Hypothetical protein FLJ40906.
Homo sapiens (Human).
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29UGB2
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                                                                                                                                                                                                                                                                                                                                                                                               RMHPNVSQGCQGGCATCSDYNGCLSCKPRLPFVLERIGMKQIGVCLSSCPSGYYGTRYPD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GERGKKG----RERKRKKLNKERKGTSSSSDSKGLBSSIETPDQQENKERQQQQKR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::|| || :| :|| || :| CQXRRKGGGGRENANRNILARKESKEAGGAGS---------RRRKGQQQQQQ 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota; Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 36.8%; Score 565.5; DB 11; Length 243; Best Local Similarity 45.8%; Pred. No. 5.2e-43; Matches 110; Conservative 36; Mismatches 83; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical thrombospondin type I repeat.
2610028F08ELK.
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32
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RESULT 8

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88 RYPDINKCTKCKVDCDTCFNKNPCTKCKSGPYLHLGKCLDSCPEGLEANNHTMECVSIVH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 CEASEWSPWSPCMKKGKTCGFKRGTETRVRDI --LQHPSAKGKGNLCPPTSETRTCIVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 RRORRMHPNVSOGCOGGCATCSDYNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
019824F16.3 (Novel protein similar to mouse thrombospondin type bJ824F16.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 29.3%; Score 450; DB 4; Length 224; Local Similarity 42.1%; Pred. No. 1.2e-32; les 88; Conservative 33; Mismatches 70; Indels
                                                                                                                                                                                                                          Blakey S.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, ALOS0125; CAB65783.3; -
Genew; HGNC:16175; C20orf182.
InterPro; IPR006812; Purin repeat.
InterPro; IPR000844; TSP1.
SWART; SM00261; FU; 2.
SWART; SM00209; TSP1; 1.
PROSTIE: PSS00209; TSP1; 1.
NON_TER 224 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg K.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027938; AAH27938.1;
InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow fac_recep.
InterPro; IPR009084; TSP1.
SMART; SM00261; FUV; 1.
SWART; SM00261; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             224 AA; 25042 MW; 97D26AD34CDBFB12 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
224 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 P--CPGERSPGQKKGRKDRRPRKDRKUDR 221
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to putative. Homo sapiens (Human)
                                                                                                                                                                                                              SEQUENCE FROM N.A.
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TISSUE=Lung;
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59 LPPFLAREGARQYGECLHSCPSGYYGHRAPDMARCARCRIENCDSCFSKDFCTKCKVGFY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Retina;
STRAIN=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CONAS.";
Nature 420:563-573 (2002).
EMBL; AK020904; BAC25643.1; -.
MGD; MGI:924467; A302028K19Rik.
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Cieplik M., Klenk H.;
Cioplik M., Klenk H.;
Cioplik M., Klenk H.;
Ciopling and functional characterization of FURIN from Spodoptera frugiperda (Sf9) cells.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S8.
--- SIMILARITY: CONTAINS I HOMO B/P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00261; FU; 2. _____SEQUENCE 138 AA; 15172 WW; FEFD7D949279D5DD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                             120 LHLGKCLDSCPEGLEANNHTMECVSIVHCEASEWS 154
                                                                                                                                         138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR006212; Furin repeat.
InterPro, IPR009030; Grow_fac_recep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z68888; CAA93116.1;
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                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A930029K19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                Q8BJ73;
                                                                                                                                                                                                                                                                                                                                                                                        Q8BJ73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          026489
                                                                                                                                                                                                                                                                                                    RESULT 11
Q8BJ73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                         SO DE L'ARTERE EN COCCO DE L'A
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KEDLINE-22388257; PubMed=12477932;

KEDLINE-22388257; PubMed=12477932;

KETAUSPERG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Budrow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Budrow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CPDGPAPLEETMECVE--GCEVGHWSEWGTCSRNNRTCGFKWGLETRTRQIVKKPV---K 115
                                                                                                                                                                                                                                                                70 MKQIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGPYLLHLGKCLDS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPFVLERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKVD-CDTCFNKNFCTKCKSGFY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                    CPEGLEANNHTMECVSIVHCEASEWSPWSPCMKKGKTCGFKRGTETRVRDILQHPSAKGK 188
                                                                                                                                                                                                                                                                                                        1 MRPCLFSFALITIACMDYSQCQ-GNRWRRNKRA-SYVSNPICKGCLSCSKDNGCSRCQQK 58
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                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 GNL-CPPTSETRTCIVQRKKCSKGERGKKGRERKRKKLNKE--ERKETSSS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : | : | : | | : | | : | | 10 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 | 110 |
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                                                                                             29.3%; Score 449.5; DB 4; Length 176;
                                                                                    Query Match
Best Local Similarity 46.8%; Pred. No. 1e-32;
Matches 80; Conservative 28; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
        20409 MW; OF83CCE1B2F8CA85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AA; 17658 MW; B74713789B2853E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 4.4e-30; 19; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUE-Egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC052844; AAH52844.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2610028F0BRik protein.
Mus musculus (Mouse).
    176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE PROM N.A.
        SEQUENCE
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8

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11

72; Gaps

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93 NKCTKCKVDCDTCP -- NKNPCTKCKSGPYLHLGKCLDSCPEGLEANNHTMECVSIVHCBA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   691 NTCVSRCPPRSFPNQVGICWPCHDTCBTCAGAGPDSCLTCAPAHLHVID-----LAVCL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745 QFCPDGYPENSRNRTCVPCEPNCASCQDHPEYCTSCDHHLVMHEHKCYSACPLDTYETED 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 SSCPSGYY-----GTRYPDI 92
                                                                                                                                                                                                                                                                                                                                                                                                        23 NASRGRRORRMHPN -- - VSQGCQGCCATCSDY -- NGCLSCKPRLPFVLBRIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE-98053888; PubMed-9393739;
Hubbard F.C., Goodrow T.L., Liu S.C., Brilliant M.H., Basset P.,
Hubbard R.C., Goodrow T.L., Liu S.C., Brilliant M.H., Basset P.,
Mains R.E., Klein-Szanto A.J.;
Wains R.E., Klein-Szanto A.J.;
With spindle cell tumor conversion and increased invasive ability.";
Cancer Res. 57:5226-5231(1997).
EMBL; AP008222; AAB95315.1; -.
MGD; MGI:102897; Pacc4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                   Query Match 11.3%; Score 174; DB 5; Length 1376; Best Local Similarity 24.5%; Pred. No. 5.2e-07; Matches 48; Conservative 15; Mismatches 61; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 171; DB 11; Length 296; 22.9%; Pred. No. 2e-07;
                                                                                                                                                                PROSITE; PS00190; CYTCHROME C; 3.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE H1S; 1.
PROSITE; PS00139; SUBTILASE SER; 1.
Hydrolase; Procease; Serine procease.
SEQUENCE 1376 AA; 149716 MW; B6704BA89BA3A88FB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006212; Purin repeat.
InterPro; IPR009030; Grow Fac_recep.
InterPro; IPR007030; IRGF.
InterPro; IPR007087; Znf_C2H2.
SWART; SM00181; BGF, 2.
SWART; SM00261; FU; 5.
PROSTIE; PS00028; ZINC_FINGER_C2H2_1; 1.
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InterPro; IPR009030; Grow fac_recep
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; Peptidase_S8B.
                                                         Pfam; PF00082; Peptidase S8; 1.
Pfam; PF01483; P_proprotein; 1.
PRINKS; PR00723; SUBTILISIN.
ProDom; PD000717; P_dmain; 1.
SNART; SM00261; PU; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 SEWSPWSPCMKKGKTC 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PACE4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCSK6 OR PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 844 CAKCHESCDICQEPGETQCVICHPSIYALDGRCVISCPPAYYADXKRKECMRCPVGCSIC 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 ------VSIVHCEASEWSPWSPCMKKGKICGFKRGIETRVRDIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 NVSQGCQGGCATCSD-YNGCLSCKPRLFFVLERIGMKQIGVCLSSCPSGYYGTRYPDINK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN Berkeley, Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         904 TSAFCLSCEPKWELNKKGKCMPVGSDKCSAGBFAVDQKCKRCNPACDSCYGEN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 12.1%; Score 185.5; DB 5; Length 1299; 1 Similarity 24.5%; Pred. No. 4.6e-08; 54; Conservative 24; Mismatches 79; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boxeryota; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                   R GO; GO:000823; Int.;

R GO; GO:000823; F:peptidase activity; IEA.

GO; GO:0004289; F:peptidase activity; IEA.

GO; GO:0004289; F:peptidase activity; IEA.

GO; GO:0005289; F:peptidase activity; IEA.

R InterPro; IPR00212; Furin repeat.

R InterPro; IPR00212; Furin repeat.

R InterPro; IPR00284; Peptidase.

R InterPro; IPR00384; Peptidase.

R InterPro; IPR00384; Peptidase.

R Pfam; PP01483; Proporotin; 1.

R Pfam; PP01483; Proporotin; 1.

R PRINTS; PR00723; SUBTILISIN.

R PROSTE; PR00134; SUBTILISEN.

R PROSTE; PS00134; SUBTILIASE ASP; 1.

R PROSTE; PS00134; SUBTILIASE ENS; 1.

R PROSTER; PS00134; SUBTILIASE ENS; 1.

R PROSTER; PS00134; SUBTILIASE ENS; 1.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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08SZS2

RESULT 13
088282
AC 088282
AC 088282
DT 01-JU
DT

Matches

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DR NA DR NA

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12;
12;
                                                            64 YPGDAAARRCRR-----CHKGCETCTGRSPAQCLSCR-RGFY-----HHQETNT 106
                                                                                                                 76 CLSSCPSGYYGTRYPDINKCTKCKVDCDTCPNK-NPCTKCKSGPYLHLGKCLDSCPEGLE 134
                                                                                                                                          135 ANNHTMEC-----PWSP 158
                                                                                                                                                                                                                         165 PDSELVKCGECHHTCRTCVGPSREECIHCAKSFHPQDWKCVPACGEGFYPEEMPGLPHKV 224
                                                                                                                                                                                                                                                                          159 CMKKGKTC----GFKRG-----TETRVRDILQHPSAKGKGNLCPPTSETRICIVQRK 206
                                                                                                                                                                                                                                                                                                              225 CRRCBENCLSCEGSSRNCSRCKAGFTQLGTSCITNHTCSNADETFCEMVKSNRLC--ERK 282
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                                        18 YIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYN--GCLSCKPRLFFVLBRIGMKQIGV 75
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72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Strausberg R.;
Strausberg R.;
Submitted (SEP-2002) to the EWEL/GenBank/DDBJ databases.
Submitted (SEP-2002) to the EWEL/GenBank/DDBJ databases.
GO; GO:0005489; P:electron transporter activity; IEA.
GO; GO:0006189; P:electron transport; IEA.
InterPro; IPR000340; CytC.heme.BS.
InterPro; IPR000212; Purin repeat.
InterPro; IPR000212; Purin repeat.
InterPro; IPR000209; Peptidase.SB.
InterPro; IPR000209; Peptidase.SB.
InterPro; IPR000209; Peptidase.SB.
InterPro; IPR000829; Peptidase.SB.
InterPro; IPR000829; Peptidase.SB.
InterPro; IPR00184; Peptidase.SB.
InterPro; IPR00184; Peptidase.SB.
IPRam; PR00483; Proprotein; I.
REMNTS; RR00717; Padomain; I.
REMNT; SM00181; RGF; S.
88; Indels
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826 AA; 91653 MW; 61BC6B49F6F42AA0 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to subtilisin-like endoprotease (Fragment).
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  25; Mismatches
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PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 1.
  55; Conservative
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159 CMKKKKTC----GPKKG-----TETRVRDILQHPSAKGKKMLCPPTSETRTCIVQRK 206
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Search completed: June 29, 2004, 17:02:18 Job time : 41.5522 secs

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inflammation disease
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N-PSDB; AAH45131.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                1586107 segs, 282547505 residues
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                                                                  OM protein - protein search, using sw model
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AAE13168
AAE13150
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AB044414
AAB13163
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ABP61846
ABR62114
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AAB93875
AAE13153
ABO44417
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geneseqp2003bs: *
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Maximum DB seq length: 200000000
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160 4 AAM79312 160 6 ABC4415 263 6 ABRC4116 263 6 ABRC21108 263 7 ABR58489 263 7 ABR58489 263 7 ABR51116 264 6 ABR62113 229 4 AAR131162 229 4 AAR37115 243 6 ABR62101 243 6 ABR62101 243 6 ABR62101 250 6 ABR62107 252 6 ABR62107 252 6 ABR62107 253 6 ABR62107 254 7 ADB76146 46 4 AAE13155	Aam79312 Human pro Aae13149 Human ste Abo44415 Human ste Abr62108 Secreted		AACALLIJ MOUBE UNT Aael3162 Mouse thr Abo44426 Mouse thr Aae37115 Human sec Abg76508 DNA encod		Abr62102 Secreted Adb76146 Novel hum Aae13155 Human SCR
	AAM79312 AAB13149 ABO44415 ARD62108	ABR621108 ABR862115 ABR8999 ADR07919 ABR62110	AB13162 AB13162 AB044426 AAB37115 ABG76508	ABR62106 AAB36166 ABR62101 ABR62107	ABR62102 ADB76146 AAB13155
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903 59.8 903 59.8 656 44.4 648.56 43.4 638 42.3 638 42.3 638 42.3 638 42.3 638 42.3 638 42.3 638 42.3 638 42.3 638 42.3 64.3 658 64.3 658 648 64.3 658 648 648 648 648 648 648 648 648 648 64	22 23 28 23 8	20000 20000 20000		8 4 4 4 5 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	4 4 4 6 4 7

ALIGNMENTS

Human; thrombospondin-30; cytostatic; anti-HIV; antiinflammatory; malignant tumour; haemopathy; HIV infection; immunological disease; (BIOR-) BIOROAD GENE DEV LTD SHANGHAI. AAB99220 standard; protein; 272 AA 27-NOV-2000; 2000WO-CN000494. 29-NOV-1999; 99CN-00124148 (first entry) Human thrombospondin-30.

Human thrombospondin-30 and polynuclectide is useful in diagnosis and treatment of, e.g., malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammatory diseases.

Claim 1; Page 27-28; 33pp; Chinese.

The present sequence is the protein sequence for human thrombospondin-30. Thrombospondin-30 protein and coding sequence are useful in the diagnosis and treatment of malignant tumour. haemopathy, HIV infection, immunological diseases and various inflammation diseases. In addition thrombospondin-30 protein may be used for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The thrombospondin-30 coding sequence may be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or in producing gene chips or microarrays

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                                                                                                                                                                  HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                              LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKOFCTKCKSGFYL 120
                                                                                                                              LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                                                                                                                                                                                          QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAIPDSKSLES 240
                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RT, Asundi V, Zhou P, Xu C, Cao Y;
Wang J, Zhang J, Ren F, Chen R, Wang ZW;
n T, Goodrich R;
                                                        1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYNGCLSCKPR
                                                                          MHLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYWGCLSCKPR
                               Gapa
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                               ö
    Length 272;
                               Indels
    DB 4;
 100.0%; Score 1510; DB 4;
100.0%; Pred. No. 1e-110;
ive 0; Mismatches 0;
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00654936.
01-SEP-2000; 2000US-00654936.
20-COT-2000; 2000US-0065351.
20-OCT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00584325.
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
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Query Match
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Matches 272; Conservative
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encoded polypeptides (AAMY8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or get stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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/note= "Human mature stem cell growth factor-like
protein"
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/label= Signal peptide
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241 SKRIPRORENKOOOKKRKVODKOKSVSVSTVH 272

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The patent discloses novel stem cell growth factor-like proteins and polymucleotides encoding them. Proteins of the invention are also known as supporting factor for the proliferation of stem cells (STR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, haematopoietic progenitor cell miltured using stem cell growth cell. The haematopoietic progenitor cell miltured using stem cell growth cell. The haematopoietic progenitor cell miltured using stem cell growth call. The haematopoietic progenitor cell miltured using stem cell growth call. The haematopoietic progenitor cell miltured using stem cell growth coll cactor-like proteins can replace as a graft for the bone marrow cord blood transplantation for treating a variety of diseases such as immunodeficiency syndrome, channed and miltips, conservation in a mucopolysaccone, agammaglobulinaemia, conservation as mucopolysacconeridosis, adrenal white matter can event as mucopolysacconeridosis, adrenal white matter can event of diseases and other neurodegenerative diseases, lromboortopaenia, immune deficiency are useful for treating diseases such as Parkinson's disease, Alzheimer's confissance and other neurodegenerative diseases, thromboortopaenia, immune deficiencies and disease such as multiple sclerosis, systemic cupus servithematosus, rheumatoid arthritis, and autoimmune disorders such as multiple sclerosis, systemic cupies miltiple manned and contained and publication and autoimmune publication arthritis, and autoimmune publication and publication and autoimmune publication and publication and publication and publication anature and publication and publication and publication and publica
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Stache-Crain B, Dickson M, Mize NK, Nishikawa M;
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09-JAN-2001; 2001US-00757562.
05-FEB-2001; 2001US-0266614P.
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(KIRI ) KIRIN BEER KK.
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N-PSDB; AAD21728.
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WO200177169-A2
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Human, stem cell growth factor-like protein, antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; osteopathic; immunodeficiency syndrome; fronic granulomatous disease; duplicated immunodeficiency syndrome; Miskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis;
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                                                                                                                                                                                                                                                                                                                                                                                                          adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
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, Nishikawa M;
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               241 SKBIPBQRENKQQQKKRKVQDKQKSVSTVH 272
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/label= Signal_peptide
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ckson M, Mize NK,
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28-UNW-2000; 2000US-0215733P.
09-JAN-2001; 2001US-0055565.
05-FRB-2001; 2001US-0266614P.
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(KIRI ) KIRIN BEER KK.
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N-PSDB; AAD21724.
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121 HIGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII

181 QHPSAKGNLCPPTNBTRKCTVQRKKCQKGBRKKRKRKRKRFNKGBSKRAIPDSKSLES

181 OHPSAKGNLCPPTNETRKCTVORKKCOKGERGKKGRERKRKKPNKGESKRAIPDSKSLES

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diseases such as immunodeficiency syndrome, chronic granulomations diseases uch as immunodeficiency syndrome, adammaglobulinaemia, wiskott-Aldrich syndrome, adammaglobulinaemia, wiskott-Aldrich syndrome, acquired immuno deficiency syndrome agammaglobulinaemia, thalassaemia, haemolyric anaemia due to enzyme deficiency syndrome (AIDS), thalassaemia, haemolyric anaemia due to enzyme defect, congenital anaemia such as sickle cell anaemia, Gaucher's disease, lysosomal storage degeneration, a variety of cancer and tumours. Proteins of the invention are useful for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from human
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transplantation or cord blood transplantation for treating a variety of
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Human; secreted; stem cell growth factor; cytostatic; haemostatic; neuroprotective; immunostimulant; leukaemia; haemophilia; cancer; degenerative disease; Alzheimer's disease; food supplement;
                                                                        Human clone 1 thrombospondin protein #23.
                                                                                                                     immunological disorder; thrombospondin.
                 ABR62112 standard; protein; 272 AA.
                                                      (first entry)
                                                                                                                                        Homo sapiens
                                                     18-AUG-2003
                                    ABR62112;
RESULT 5
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30-AUG-2001; 2001US-0316368P. 10-DEC-2001; 2001US-0339739P. 19-APR-2002; 2002US-00125852. 30-AUG-2002; 2002WO-US027746. (HYSE-) HYSEQ INC WO2003029405-A2 10-APR-2003.

Tang YT;

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The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. cantile stem cells to generative diseases like Alzheimer's compared in the management of the polyneries are also useful for generating met tissues and organs that can applied transplanted tissues. The polynucleotides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in concombinantly producing protein, in comparating antisense DNA or RNA, in diagnostics as expressed sequence tags for identifying expressed genes, and for inducing immune response. The polypeptides are useful for generating antibodies that specifically bind the polypeptide, as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the current cor prevention of cancers, and other immunological disorders. The current expensence represents a human clone I thrombospondin protein
                                                                     useful
                                                                     New stem cell growth factor-like polypeptides and polynucleotides, use for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.
                                                                                                                                                                                   Disclosure, Fig 1; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 272 AA;
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180 180 240 191 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKRAIPDSKSLES 240 61 LFPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120 61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120 9 1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQCQGGCATCSDYNGCLSCKPR 121 HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREII 181 OHPSAKGNI,CPPTNETRKCTVORKKCOKGERGKKGRERKRKKPNKGESKRAIPDSKSLES 1 MHIRLISWILFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR 0; Gaps Indels DB 6; ; Score 1510; DB 6; Pred. No. 1e-110; 0; Mismatches 0 Query Match 100.0%; Best Local Similarity 100.0%; Matches 272; Conservative 0. a ð 유 요 Š ઠ 8

Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; heamatopoietic progenitor cell; stromal cell; AIDS; thalassesemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Wiskott-Aldrich sydrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; Human stem cell growth factor-like protein, SCR 1 #4. ABO44432 standard; protein; 272 AA 30-SEP-2003 (first entry) RESULT 6 ABO44432

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TANG Y T.
                    US2003044792-A1.
                                                     N-PSDB; ACH04328
                                             CHAO C.
     Homo sapiens
                       06-MAR-2003
                                                rang YT,
         Peptide
                                       (DRMA/)
(MIZE/)
(NISH/)
(CHAO/)
             Protein
                                    TANG/)
                                      LABA/)
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The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 for its mature protein portion, or fragment, analogue, variant or SCR-1 polymucleotide, a most cell growth factor activity, or the complement of the polymucleotide, a most cell growth factor activity or the SCR-1 polymucleotide, a most cell growth a regulatory sequence of SCR-1 polymucleotide in operative association with a regulatory sequence CSCR-1 polymucleotide in operative association with a regulatory sequence comprising the SCR-1 polymucleotide (the polypeptide which is an proparation of the SCR-1 polymucleotide (the polypeptide which is an controls expression product of the SCR-1 polymucleotide (the polypeptide which is an control expression product of the SCR-1 polymucleotide (the polypeptide which is an activity to support progenitor cell, with a proviso that C-terminal as a collecting any 10 consecutive as from ABO44430, an isolated polypeptide or sequence does not comprise the as equence appearing as ABO44433 and ABO44430, an isolated polypeptide consintain survival of or promote proliferation of a stem cell or germ cell, an anti-SCR-1 antibody, a mucleic acid array comprising the SCR-1 polymucleotide or a unique segment of the SCR-1 polymucleotide or a unique segment of polypeptide attached to a surface, a stromal cell genetically engineered to express the SCR-1 polymucleotide or a unique segment of polypeptide attached to a surface, a stromal cell genetically engineered to express the SCR-1 polymous account in a management of the SCR-1 polymous or survival of a stem cell or germ cell and an implant comprising a cell companies attached to a surface, a stromal cell genetically engineered to express the SCR-1 polymous or survival of a stem cell or germ /note= "Mature stem cell growth factor-like protein. This protein is specifically claimed in claim 9° Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. Chao C; Labat I, Drmanac RT, Mize N, Nishikawa M, label= Signal_peptide Location/Qualifiers Claim 23; Page 82; 96pp; English. 28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 05-APR-2001; 2001US-0282397P. 28-JUN-2001; 2001US-00894912 LABAT I. DRMANAC R T. MIZE N. NISHIKAWA M. 2003-625403/59

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healing. The human haematopoietic stem cell or human haematopoietic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, ALDS, etc., thalassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth, sustaining neuronal populations, cartilage remodeling, bone growth, and immunosuppression. The present sequence is a Human SCR-1
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                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1510; DB 6; Length 272; 100.0%; Pred. No. 1e-110; ive 0; Mismatches 0; Indels 0.
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Matches 272; Conservative 0
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        Sequence 272 AA;
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ပံ

Chao

Drmanac RT, Mize N, Nishikawa M,

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05-APR-2001; 2001US-0282397P
      DRMANAC R T.
MIZE N.
NISHIKAWA M.
               Labat I,
   TANG Y T.
     LABAT I.
            CHAO C.
               Fang YT,
        (MIZB/)
(NISH/)
                                                                                                                   protein
            (CHIAO/)
     LABA/
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The invention relates to an isolated stem cell growth factor-like polyperide (referred as supporting factor for proliferation of stem cells (SCR-1) from mouse or human, or its mature protein portion, or tragement, analogue, variant or carrivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion or fragement, analogue, variant or carrivative, that retains stem cell growth factor activity or the complement of the polymucleotide, a host cell growth factor activity or the complement of the polymucleotide, a host cell growth factor activity or the complement of the polymucleotide, a polypeptide or comprising the SCR-1 polymethed or carrivation with a regulatory sequence of the SCR-1 polymethed or all state of the polymucleotide in the host cell, preparation of the SCR-1 polymethed a polypeptide which is an activity to support proliferation or survival of hasmatopoietic stem cell corput factor cell, with a provise that cereminal and activity to support proliferation or survival of consecutive as from ABO44430, an isolated polypeptide will an exting any 10 consecutive as from ABO44430, an isolated polypeptide will an exting any 10 consecutive as from ABO44430, an isolated polypeptide will an extended some antended or a surface, as tromal engineers of cell or germ cell and an implant comprising the SCR-1 polymetleotide or a unique segment of the SCR-1 polymetleotide or a unique segment of the SCR-1 polymetleotide and an implant comprising the SCR-1 polymetleotide or aupport proliferation or centraling the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising or cell or germ cell and an implant comprising or cell or sprease the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant or survival of a stem cell or germ cell and an implant or survival of a stem cell or germ cell and an implant or cell rangement or cell certain definition w
                                                                            Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cells.
                                                                                                                                                                                                                                                                                                                                             Claim 23; Fig 3; 96pp; English.
                                        N-PSDB; ACH04323, ACH04324.
WPI; 2003-625403/59
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Gaps

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Query Match 100.0%; Score 1510; DB 6; Length 272; Best Local Similarity 100.0%; Pred. No. 1e-110; Matches 272; Conservative 0; Mismatches 0; Indels 0;

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Human; stem cell growth factor-like protein; antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliaer; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immunodeficiency syndrome; agammaglobulinaemia; thalassaemia; Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                 191 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKRDNKGESKEAIPDSKSLES 240
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                                                                                         61 LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNRNPCTKCKSGFYL 120
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                       1 MHLRLISWLFIIIANFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
MILLALI SWLPI I LINPMEY I GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
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ckson M, Mize NK, Nishikawa M;
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28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-00757562.
05-FEB-2001; 2001US-0266614P.
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Dickson M,
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(KIRI ) KIRIN BEBR KK.
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The patent discloses movel stem cell growth factor-like proteins and compared to the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, emronic stem cell, parametopoietic stem cell, mbryonic stem cell, parametopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell pluripotent cell growth cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth care proteins can replace as a graft for the bone marrow cell growth cell seases such as immunodeficiency syndrome, chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immuno deficiency syndrome (hins), thatassaemia, haemolytic anaemia due to enzyme defect, congenital anaemia cell seases such as mucopolysaccharidosis, adrenal white matter cell are assible cell anaemia diseases such as parkinson's diseases, Alzheimer's diseases con treating diseases such as Parkinson's disease, Alzheimer's diseases and tumours. Proteins of the invention of diseases such as Parkinson's disease, Alzheimer's diseases of Alzheimer's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCID)) and autoimmune disorders such as multiple sclerosis, systemic upus erythematosus, theumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy. The present sequence is stem cell growth factor-like protein from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency
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Chao C;

Tang YT, Labat I, Drmanac RT, Mize N, Nishikawa M,

WPI; 2003-625403/59.

05-FEB-2001; 2001US-0266614P.

DRMANAC R T. NISHIKAWA M. CHAO C.

MIZE N.

(MIZB/) LABA/) (DRMA/)

(NISH/) (CHAO/)

TANG Y T.

(TANG/)

LABAT I.

2000US-0215733P.

28-JUN-2000;

28-JUN-2001; 2001US-00894912.

US2003044792-A1

06-MAR-2003.

Homo sapiens.

63 FPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNNPCTKCKSGFYLH 122 123 LGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 182 122 JGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQ 181 62 61 3 HLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGGCGATCSDYNGCLSCKPRL 2 HLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL 62 FPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH HPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEAI PDSKSLESS Gaps ö 99.7%; Score 1505; DB 4; Length 273; 100.0%; Pred. No. 2.5e-110; ive 0; Mismatches 0; Indels 0 243 KEIPEGRENKQQKKRVQDKQKSVSVSTVH 273 242 KEIPBORENKOOOKKRKVODKOKSVSVSTVH 272 Query Match Best Local Similarity 100. Matches 271; Conservative 182 Best Loca. Matches è 셤 윱 윱 ઠે 셤 ઠ 日 ð

Human stem cell growth factor-like protein, SCR 1 #2. ABO44414 standard; protein; 273 AA. 30-SEP-2003 (first entry) RESULT 9 4B044414

The invention relates to an isolated stem cell growth factor-like polypeptide (Ireferred as supporting factor for proliferation of stem coll pypeptide (Ireferred as supporting) are not in solated polymerleding of factor activity. Also included are an isolated polymerleding stem cell growth factor activity, or the charvative, that retains stem cell growth factor activity, or the derivative, that retains stem cell growth factor activity, or the carpinal stem cell growth factor activity, or the campinal as the polymerledide, an (expression) vector comprising the SCR-1 polymerledide in operative association with a regulatory sequence that controls expression of the polymerledide with a regulatory sequence. SCR-1 polymerledide in operative association with a regulatory sequence that controls expression of the polymerledide (the polypeptide special polymerledide with stem coll or preparation of the SCR-1 polymerledide (the polypeptide special polypeptide with stem cell crowth factor cell, with a proviso that C-terminal as sequence does not comprise the as sequence appearing as ABG44438 and ABG44438 and ABG44438 and ABG44438 and ABG44438 and ABG44439, a culture medium comprising the SCR-1 polypeptide with stem cell growth factor activity having at least an as sequence appearing as ABG44438 and ABG44438 and ABG44439, a culture medium comprising the SCR-1 polypeptide to maintain survival of or promote proliferation of a stem cell or germ cell, an anti-SCR-1 antibody, a mucleic acid array comprising the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell or Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor Claim 23; Page 72-73; 96pp; English. N-PSDB; ACH04325 241 121 Stem cell growth factor-like protein; antianemic; anti-HIV; SCR-1; immunostimulant; vulnerary; haematopoietic stem cell; gene therapy; supporting factor for proliferation of stem cells; wound healing; haematopoietic progenitor cell; stromal cell; AIDS; thalassaemia; bone marrow transplantation; cord blood transplantation; cord blood transplantation; cord blood transplantation; agammaglobulinemia; Wiskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; Gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human.

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morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth, sustaining neuronal populations, cartilage remodeling, bone growth and immunosuppression. The present sequence is a Human SCR-1
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                                                                                                                                                                                                                                                                                                                                                   HPSAKGNI, CPPTWETRKCTVQRKKCQKGERGKKGRERKRKKPWKGESKRAIPDSKSLESS 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stem cell growth factor-like protein; antiinflammatory; nootropic;
                                                                                                                                                                                                                                 62
                                                                                                                                                                                                  2 HLRLISWLFIILNPMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; vilnerary; cytostatic; anticonvulsant; immunostimulant; vasotropic; virucide; dermatological; tranquilliser; cerebroprotective; ossteopethic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; Albs; acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; Albs; acquired immunodeficiency syndrome; wiskott-Aldrich syndrome; thalbs; aducher's disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; all sease; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; thrombocytopaenta; SCID; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammaction; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell; secreted protein.
                                                                                                                                                                                                                     HLRLISWLPIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGCATCSDYNGCLSCKPRL
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                                                                                                                                Length 273;
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                                                                                                                                  Score 1505; DB 6; L
Pred. No. 2.5e-110;
                                                                                                                    99.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEI PEQRENKQQQKKRKVQDKQKSVSVSTVH 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB13163 standard; protein; 265
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28-JUN-2000; 2000US-0215733P.
09-JAN-2001; 2001US-0075562.
05-PEB-2001; 2001US-026614P.
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                                                                                                                                                                 Matches 271; Conservative
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                                                                                                                              Query Match
Best Local Similarity
                                                                                                    Sequence 273 AA;
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(KIRI )
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The parent unscribes inversariant to the invention are also known as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell or germ cell which is preferably primordial germ cell, germ line stem cell, embryonic stem cell, haematopoietic stem cell, haematopoietic progenitor cell, pluripotent cell, nate to totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, cell or totipotent cell. The haematopoietic progenitor cell. The bone marrow factor-like proteins can replace as a graft for the bone marrow cell sease, duplicated immunodeficiency syndrome, chronic granulomatous disease, duplicated immunodeficiency syndrome, agammaglobulinaemia, wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS), cuch as sickle cell anaemia, Gaucher's disease, lysosomal storage chiseases such as mucopolysaccharidosis, adrenal white matter cell anaemia, daucher's disease, lysosomal storage deficiency avaiety of cancer and tumours. Proteins of the invention are useful for treating diseases such as severe combined immune deficiency contraction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCID)) and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune pulmonary inflammation. Sequences of the invention are also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                              Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELRISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQCQGGCATCSDYMGCLSCKPR
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                                                                                                                                                                                                                              patent discloses novel stem cell growth factor-like proteins and
RT;
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  Liu C,
  Sinku A, Liu
Nishikawa M;
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100.0%; Pred. No. 3.8e-108;
ive 0; Mismatches 0;
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  Labat I, Tillinghast JS, S.
In B, Dickson M, Mize NK,
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                                                                                                                                                                                     Disclosure; Fig 3; 232pp; English
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Best Local Similarity 100.1
Matches 265; Conservative
                                                              WPI; 2001-657166/75.
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healing. The human haematopoletic stem cell or human haematopoletic progenitor cell culture using the SCR-1 polypeptide can replace as a graft for the conventional bone marrow transplantation or cord blood transplantation. The transplantation of haematopoietic stem cells can be employed as a therapy for treating diseases such as chronic granulomatous diseases, duplicated immunodeficiency syndrome, agammaglobulinaemia, Miskott-Ahdrich syndrome, AlDS, etc., thalassaemia, haemolyric anaemia due to enzyme defect, congenital anaemia such as sicklaemia, Gaucher's disease etc. the SCR-1 polypeptide is useful for cell growth and morphogenesis, including tissue specific stem cell growth, epithelial cell growth and regulation, ovarian follicle development, promoting nerve cell growth and immunosuppression. The present sequence is a protein homologous to Human SCR-1 protein

The invention relates to an isolated stem cell growth factor-like polypeptide (referred as supporting factor for proliferation of stem cells (SCR-1)) from mouse or human, or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity. Also included are an isolated polymucleotide encoding SCR-1 (or its mature protein portion, or fragment, analogue, variant or derivative, that retains stem cell growth factor activity, or the complement of the polymucleotide), an (expression) vector comprising the SCR-1 polymucleotide in host cell genetically engineered to contain the SCR-1 polymucleotide in operative association with a regulatory sequence SCR-1 polymucleotide in the host cell, the controls expression of the polymucleotide in the host cell, preparation of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide having an expression product of the SCR-1 polymucleotide (the polypeptide tem cell, vith a proviso that C-terminal as sequence does not comprise the as sequence appearing as ABO4443), an solated SCR-1 polypeptide with stem cell growth factor activity and cloaked SCR-1 polypeptide with stem cell growth factor activity and sequence appearing as ABO44428 and ABO44429, a culture medium comprising the SCR-1 polypeptide or a unique segment of the SCR-1 polypeptide or a unique segment of the SCR-1 polymucleotide or a stromal cell growth factor activity and cell or maintain survival of or promote proliferation of a stem cell or served to the screen of a stromal cell segment of the SCR-1 polymucleotide or a stromal cell served by served to surface, a stromal cell served by served by served to surface to served by served by serve engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell and an implant comprising a cell genetically engineered to express the SCR-1 polypeptide to support proliferation or survival of a stem cell or germ cell. The SCR-1 polypeptide is useful for identifying a compound that binds to the SCR-1 polypeptide and for maintaining survival of or promoting proliferation of a stem cell, a germ cell, a germ cell, a permention of progenitor cell, a germ cell, a polypeptide is useful for promoting wound 28-JUN-2000; 2000US-0215733P. 05-FEB-2001; 2001US-0266614P. 28-JUN-2001; 2001US-00894912. LABAT I. DRMANAC R T. NISHIKAWA M. WPI; 2003-625403/59. fang YT, Labat I, TANG Y T. US2003044792-A1 MIZE N. CHAO C. Homo Bapiens 06-MAR-2003 (MIZE/) (NISH/) (TANG/) CHIAO/ (LABA/) (DRMA/)

immunostimulant; vulnerary; hematopoietic stem cell; gene therapy; immunostimulant; vulnerary; hematopoietic stem cells; wound healing; haematopoietic progenitor cell; stromal cell; halbs; thalassaemia; bone marrow transplantation; cord blood transplantation; chronic granulomatous disease; duplicated immunodeficiency syndrome; agammaglobulinaemia; Miskott-Aldrich syndrome; haemolytic anaemia; congenital anaemia; sicklaemia; gaucher's disease; morphogenesis; epithelial cell growth; ovarian follicle development; nerve cell growth; cartilage remodeling; bone growth; immunosuppression; human. Novel isolated polypeptide having stem cell growth factor activity, useful for promoting wound healing, and as a medicine to proliferate or support human hematopoietic stem cells or human hematopoietic progenitor cell growth factor-like protein; antianemic; anti-HIV; SCR-1; Nishikawa M, Mize N, Disclosure; Pig 3; 96pp; English. Drmanac RT,

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                                                                                                                                                                                                97.8%; Score 1477; DB 6; Length 265; 100.0%; Pred. No. 3.8e-108; ive 0; Mismatches 0; Indels
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98US-00065125.
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                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                           Sequence 265 AA;
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                                                                                                                                                                                                                                                                                                                                           121
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of clones ci254 (AAV83132), da2286 (AAV83133), du4105 (AAV83134), eh801 (AAV83135), er3601 (AAV83136), fimed1 (AAV83139) or fr4732 (AAV83139), call clones are deposited as ATCC 98415) and the proteins they encode are predicted to have biological activities which would make them suitable for treating, preventing or amellorating medical conditions in humans and animals for example, tumour suppression/invasion activity, immune system boosting activity. The polynucleotides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, stem cell growth factor-like protein, antiinflammatory; nootropic; neuroprotective; vulnerary; cytostatic; anticonvulsant; immunostimulant; assotropic, virucide; dermatological; tranquillilaer; cerebroprotective; osteopathic; immunodeficiency syndrome; chronic granulomatous disease; duplicated immunodeficiency syndrome; wiskott-Aldrich syndrome; AIDS; acquired immuno deficiency syndrome; wiskott-Aldrich syndrome; AIDS; daucher; disease; lysosomal storage disease; mucopolysaccharidosis; adrenal white matter degeneration; anaemia; neurodegenerative disease; Parkinson's disease; thrombocytopaenia; SCID; severe combined immunodeficiency; immune disorder; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1; supporting factor for the proliferation of stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLGKCLDNCPEGLEANNHTMECYSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
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                                    New polynucleotides encoding secreted human proteins - are derived from human foetal brain, adult brain, adult blood or placenta cDNA libraries, useful, e.g. as potential immunomodulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHLRLISWLFIILNPMEYIGSQNASRGRRQRRWHPNVSQGCQGCATCSDYNGCLSCRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKBA I PDSKSLBS
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                                                                                                                                                         nucleotide sequence (NS) of the full-length protein-coding
                                                                                                                                                                                                                                                                                                                                                                                            Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Pred. No. 4.3e-108;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                believed to be useful for gene therapy
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                                                                                                                  Claim 8; Page 63-64; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 265; Conservative
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Best Local Similarity
N-PSDB; AAV83133
                                                                                                                                                                                                                                                                                                                                                   Sequence 292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2002
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Novel stem cell growth factor like polypeptides and polynucleotides for identifying modulators useful for treating diseases such as Alzheimer's disease, cancer, rheumatoid arthritis, osteoporosis.

Claim 27; Page 231-232; 232pp; English.

Drmanac RT;

Labat I, Tillinghast JS, Sinku A, Liu C, ain B, Dickson M, Mize NK, Nishikawa M;

WPI; 2001-657166/75. N-PSDB; AAD21740.

Stache-Crain B,

ĭ Tang

05-APR-2000; 2000US-00543774. 28-JUN-2000; 2000US-0215733P. 09-JAN-2001; 2001US-00757562. 05-FBB-2001; 2001US-0266614P.

(KIRI) KIRIN BEBR KK

(HYSE-) HYSEQ INC.

05-APR-2001; 2001WO-US011208

18-0CT-2001

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The patent discloses novel stem cell growth factor-like proteins and as supporting factor for the proliferation of stem cells (SCR-1). Stem cell growth factor-like proteins of the invention are also known cell growth factor-like proteins are useful for supporting proliferation or cell growth factor-like proteins are useful for supporting proliferation or survival of a stem cell, embryonic stem cell, germ cell, paramatopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell, pluripotent cell or totipotent cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic progenitor cell cultured using stem cell growth cell. The haematopoietic can replace as a graft for the bone marrow cord blood transplantation for treating a variety of disease such as immunodeficiency syndrome, agammaglobulinaemia.

Wiskott-Aldrich syndrome, acquired immune deficiency syndrome (hibS). thalassacmia, haemolytic anaemia due to enzyme defect, congenital anaemia cell seases such as miltiple solf manune cell storage diseases und a variety of cancer and tumours. Proteins of the invention cell sease and other neurodegenerative diseases, thrombocytopaenia, immune deficiencies and disorders such as severe combined immunodeficiency collupus erythematosus, rheumatoid arthritis, and autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and autoimmune such cell in gene therapy.

Che present sequence is human SCR-1 related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKRFCTKCKSGFYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 QHPSAKGNLCPPTNBTRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKRAIPDSKSLBS
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100.0%; Pred. No. 4.3e-108;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 265; Conservative
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WO200177169-A2

protein;

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The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary decyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or prevention of tumoures. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activity and inhibin-related cytokines. (I) can be used to manipulate stem cells in culture to give crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis. (I) is involved in chemotactic or chemokinetic artifuctor regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
                                                                                                                                                                                                                                       Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antinflammatory; antibacterial; immunosuppressive; antiparkinsonian; meuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; neuropathy; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted or transmembrane protein and polymucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins-Racie LA,
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SKEI PEORENKOOOKKRKVODKOKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lavallie ER,
Spaulding V;
                                                                                         ABP61846 standard; protein; 292 AA
                                                                                                                                                                                                       Human polypeptide SEQ ID NO 200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-2000; 2000US-00745763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00040963
                                                                                                                                                                   04-OCT-2002 (first entry)
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N-PSDB; ABQ92060.
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MERBERG D.
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LAVALLIB E
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(SPAU/)
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                                                        RESULT 14
                                                                         ABP61846
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and for regeneration of bone, cartilage, tendon, ligament and/or nervetissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoprosis, osteoarthritis, bone degenerative disorders or periodontal disease. (1) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polypeptide of the invention ö 240 120 120 180 180 240 9 9 1 MHLRLISWLFIILNFWRYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 61 LFFALERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 121 HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREII OHPSAKGNI-CPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKEAIPDSKSLBS 181 QHPSAKGHLCPPTMETRKCTVQRKKCQKGERGKKGRERKRKKPNKGBSKGAIPDSKSLES 1 MHIRLISWLFIILNFWBYIGSQNASRCRRQRRWHPNVSQCQGGGATCSDYNGCLSCKPR LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGPYL Gaps Human; secreted; stem cell growth factor; cytostatic; haemostatic; neuroprotective; immunostimulant; leukaemia; haemophilia; cancer; degenerative disease; Alzhelmer's disease; food supplement; . Length 292; 97.8%; Score 1477; DB 5; Length 2 100.0%; Pred. No. 4.3e-108; ive 0; Mismatches 0; Indels Human secreted protein clone da_288_6 #25. 241 SKEIPEQRENKQQQKRRKVQDKQKS 265 241 SKEIPEQRENKQQQKKRKVQDKQKS 265 ABR62114 standard; protein; 292 AA 30-AUG-2001; 2001US-0316368P. 10-DEC-2001; 2001US-0339739P. 19-APR-2002; 2002US-00125852. 30-AUG-2002; 2002WO-US027746. (first entry) 265; Conservative immunological disorder Similarity (HYSE-) HYSEQ INC Sequence 292 AA; WO2003029405-A2. sapiens 18-AUG-2003 .0-APR-2003. Query Match Best Local S 61 121 ABR62114; rang YT; RESULT 15 ABR62114 Matches 888888888888888888 8 g 8 셤 셤 셤 ð ð ð

WPI; 2003-381616/36.

New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia and degenerative diseases like Alzheimer's disease, and for inducing immune response.

Disclosure; Fig 2; 151pp; English.

The invention relates to new stem cell growth factor-like polypeptides and polynucleotides. The stem cell growth factor-like polypeptides and polynucleotides are useful for inducind differentiation of embryonic and adult stem cells to give rise to different cell types, for treating e.g. leukaemia, haemophilia and degenerating different cell types, for treating e.g. leukaemia, haemophilia and degenerating use tissues and organs that considers are also useful for generating new tissues and organs that may aid patients in need of transplanted tissues. The polynucleotides are useful as hybridisation probes, oligomers or primers for PCR, for chromosome and gene mapping, in recombinantly producing protein, in continuous and sense and for inducing immune response. The polypeptides are useful for generating antibodies that specifically chind the polypeptides are useful for generating antibodies that specifically chind the polypeptides as molecular weight markers, and as a food supplement (e.g. protein or amino acid supplement, and as a carbon, nitrogen or carbohydrate source). Compositions comprising the polypeptides or polymucleotides are useful for the diagnosis, treatment or prevention of cancers, and other immunological disorders. The current sequence represents a human secreted protein clone da_288_6

Sequence 292 AA;

LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNNNFCTKCKSGFYL 120 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREII 180 121 HIGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKRAIPDSKSLES 240 Gaps ö Length 292; 0; Indels 97.8%; Score 1477; DB 6; Li 100.0%; Pred. No. 4.3e-108; vative 0; Mismatches 0; 241 SKRIPEORENKOOOKKRKVODKOKS 265 SKEIPEORENKOOOKKRKVODKOKS 265 Query Match Best Local Similarity 100. Matches 265; Conservative 61 19 121 181 181 셤 ò g 쉱 ð 8 g 셤 કે ठे

rch completed: June 29, 2004, 16:59:53 time : 50.5178 secs Search Job tim 2, Appli 10, Appli 10, Appli 10, Appli 10, Appli 10, Appli 10, Appli 4, Appli 2, Appli

Appli Appli Appl

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18 YIGSONASRGRRORRMHPNVSQGCQGGCATCSD--YNGCLSCXPRLFFALBRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08284941
; Sequence 2, Application US/08284941
; Patent No. 5863756
; GENERAL INPORMATION:
   APPLICANT: BARR, PHILIP J
; APPLICANT: KIERER, MICHABL C
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
   ADDRESSE: ADDRESS:
   ADDRESSE: ADDRESS:
   ADDRESSE: ADDRESS:
   CITY: PALO ALTO
   STREET: PALO ALTO
   STREET: CALIFORNIA
   COUNTRY: USA
   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-640-173-186
US-09-713-550-186
US-09-713-550-186
US-09-113-825-2
US-08-89-232-2
US-09-132-769-3
US-09-132-769-5
PCT-US93-03164-10
US-08-857-076-103
US-08-857-076-103
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US-08-857-076-103
US-08-858-864-6418-18
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.8
Matches 44; Conservative
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; MOLECULE TYPE: protein
US-08-284-941-2
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1510
1 MHLRLISWLPIILNPMBYIG.....QQKKRKVQDKQKSVSVSTVH 272
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Sequence 21,
Sequence 21,
Sequence 18,
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Sequence 2,
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Sequence 7
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2: /cgn2 6/ptcdata/2/iaa/5B COMB.pep:*
3: /cgn2 6/ptcdata/2/iaa/6A COMB.pep:*
/cgn2 6/ptcdata/2/iaa/6B COMB.pep:*
5: /cgn2 6/ptcdata/2/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptcdata/2/iaa/PCTUS COMB.pep:*
                          GenCore vergion 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-976-838-23
US-08-976-838-21
US-08-976-838-18
US-08-976-838-18
US-09-214-555B-2
US-09-214-555B-2
US-09-907-794A-4
US-09-905-125A-4
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US-09-132-769-1
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                                                                                                                                                                                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Result

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Gaps

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ZIP: 94306
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                                                                                                                                                                                                       Sequence 2, Application US/08447642
Patent No. 5989800
GENERAL INPORMATION:
APPLICANT: BARN, PHILIP J
APPLICANT: RIBPER, MICHAEL C
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCES 16
CORRESPONDENCE ADDRESS:
ADDRESSE: COOLEY GOOWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUMTRY: USA

ZIP: 94306

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FLING DATE: 23-MAY-1995
CLASSIFICATION NUMBER: US 08/284,941
PRICK APPLICATION NUMBER: US 08/284,941
PLING DATE: 2 August 1994
ATYORNEY/AGENT INFORMATION:
NAME: REGILEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
                                                                           135 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 167
                                                                                                                 ---TCG 853
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TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ILRUGTH: 969 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 969 amino acids
amino acid
                                                                                                               838 PDSELIRCGECHH---
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                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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nes 44, Conserv
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Matches 44
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RESULT 3 US-09-236-503-2

78;

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563 GHYHADK-KRCRKCAPN-----CESCPGSHGDQCMSCKYGYPL-----NEETINSCV 607
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                                                                                                                                                                                                                                                                                 665 GQDCQPCHRFCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYFDHSSENGYKSCKKC 724
                                                                                                                                                                                                                                                                                                                                             13.7 NHTMB-----NPWSPCTKK 162
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                                                                                                                                                                   20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROFEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Ross P.C.
                                                                                  10.7%; Score 162; DB 2; Length 799; 22.3%; Pred. No. 9.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 799;
                                                                                                                        81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 162; DB 2; 22.3%; Pred. No. 9.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.3%; Pred. no.
                                                                                                                           33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSER: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08976838
Patent No. 5981259
                                                                                                                                                                                                                                                                                                                                                                                                                              163 GKTC-----GPKRGTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 2848
REPERENCE/DOCKET NUMBER: 2848
TELECOMMUNICATION INFORMATION:
TELEFROM: (303) 863-9700
TELEFRAX: (303) 863-9700
INPORMATION FOR SEQ. ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                Query Match
Best Local Similarity 22.3#
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 799 amino acida
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein
US-08-976-838-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 QRKKCQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               783 QRKVLQQ 789
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Best Local Similarity
Matches 55; Conserva
  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                          US-08-525-940-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           737 YPGDTAARRCRR-----CHKGCBTCSSRAATQCLSCR-RGFY-----HHQEMNT 779
                                                                                                                                                                                                                                                                                                                                           18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFFALERIGMKQIGV
                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                          DB 5; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
OVERESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        11.5%; Score 173.5; DB 5; Length 28.8%; Pred. No. 1.3e-06; rative 16; Mismatches 54; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 ANNHIMECVSIVHCEVSEWNPWSPCTKKGKTCG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07-015-19-3
ATTORNEY/AGENT INFORMATION:
NAME: CONNEIL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 863-0223
INFORMATION POR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08525940 Patent No. 5866351
               TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-0663
TELEX: 380816 CCOLLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
TYPE: amino acids
TYPE: 1nnear
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                  44; Conservative
                                                                                                                                                                                MOLECULE TYPE: protein PCT-US93-02147A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               838 FDSELIRCGECHH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Denver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80203
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137 NHTME-----NPWSPCTKK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        645 GHYHADK-KRCRKCAPN-----CESCFGSHGDQCMSCKYGYFL-----NEBTNSCV
20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLPPALBRIGMKQIGVCL
                                                                              78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLPPALBRIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.7%; Score 162; DB 2; Length 881;
Best Local Similarity 22.3%; Pred. No. 1.1e-05;
Matches 55; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERRINGL/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-023
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-976-838-21
; Sequence 21, Application US/08976838
; Patent No. 5981259
                                                                                                                                                                                                                                            163 GKTC-----GPKRGTB----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          881 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       202 QRKKCQK 208
                                                                                                                                                                                                                                                                                                                                                            865 QRKVLQQ 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-976-838-21
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                                                                                                                                                                                        665 GQDCQPCHRFCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYFDHSSENGYRSCKKC 724
                          GHYHADK-KRCRKCAPN------CESCPGSHGDQCMSCKYGYPL-----NBETNSCV 607
                                                                                78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 136
                                                                                                       13.7 NHTME-----NPWSPCTKK 162
                                                                                                                                                                                                                                            ---TRVREIIQHPSAKGNLCPPTNETRKCTV 201
                                                                                                                                                                                                                                                                                 725 DISCLICNGPGFKNCTSCPSGYLLDLGMCQMGAICKDATBESWAEGGFCMLVKKNNLC-- 782
    GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGWKQIGVCL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTB PROTEASES AND GENES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDERR: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
PILING DATE: 07-JUL-1993
APPLICATION NUMBER: US 08/088,322
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            163 GKTC-----GPKRGTB------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08525940 Patent No. 5866351 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 22.3
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-525-940-21
                                                                                                                                                                                                                                                                                                                         QRKKCQK 208
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STREET: 17
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US-08-525-940-21
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--IVHCEVSEW-----NPWSPCTKK 162
                                                                         -TRVREIIQHPSAKGNLCPPTNETRKCTV 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 NHTME-----NPWSPCTKK 162
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                                                                                                                                                                                                                                                                                       Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES:
ADDRESSER: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENY APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 162; DB 2;
22.3%; Pred. No. 1.1e-05;
tive 33; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION UNDRER: 32,020
REFERENCE/DOCKET UNDRER: 2848-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAK: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                            163 GKTC-----GPKRGTB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915 amino acids
amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                          202 QRKKCQK 208
                                                                                                                                                                                             899 QRKVLQQ 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
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137 NHTMB---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80203
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                                                                                                    SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 136
13.7 NHTME-----NPWSPCTKK 162
                                                                         163 GKTC-----GPKRGTE-----TRVREIIQHPSAKGNLCPPTNBTRKCTV 201
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-UL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08525940; Patent No. S866351; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
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                                                                                                                                                        202 QRKKCQK 208
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es 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Denver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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202 QRKKCQK 208
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APPLICANT: INNOTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILE REFERENCE: PRO-PROTEIN CONVER ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT PILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR PILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VOR: 2.1
                                                                                                                            Sequence 2, Application US/09214555B

Patent No. 6380171

GENERAL INFORMATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING
TITLE OF INVENTION: PRO-PROTEIN CONVERTING
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT FILING DATE: 1999-01-04
PRIOR FILING DATE: 1996-07-26
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VER. 2,21
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; Patent No. 6380171
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
202 ORKKCOK 208
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                                     899 QRIKVLÓQ 905
                                                                                                                  US-09-214-555B-2
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US-09-214-555B-7
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LENGTH: 915
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324 THCPDGSYQDTKK---NLCRKGSENCKTCTEFHNCTECRDGLSLQGSRCSVSCEDGRYFN 780
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                                                                                                                                                                     78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGPYLHLGKCLDNCPEGLEAN 136
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                                                                78; Gaps
                                                                                                                           20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL
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10.7%; Score 161; DB 1; Length 288;
Best Local Similarity 28.2%; Pred. No. 3.8e-06;
Matches 46; Conservative 25; Mismatches 52; Indels
Query Match 10.7%; Score 162; DB 4; Length 915; Best Local Similarity 22.3%; Pred. No. 1.1e-05; Matches 55; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Franzusoff, Luis R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: RNCODING SAID PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER 19220
COMPUTER FIORPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
ATORIAN NUMBER: US/08/368,852
FILING DATE: O5-JAN-1995
CLASSIFICATION NUMBER: US/08/368,852
ATORIXYARA/AGSHT INPORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 37,459
TELEPHONE: 303/863-9700
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08368852 Patent No. 5691183
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INFORMATION FOR SEQ ID NO: 15:
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amino acid
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CURRENT APPLICATION NUMBER: US/09/905,125A
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Best Local Similarity 24.99
Matches 60; Conservative
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Sao, Wei-Qiang
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Baton, Dan L.
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                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                      93 NKCTKCKADCDTCPNK--NPCTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSIVHC 148
                                                                             -- 112
13 PECSEVGCDGPGPDHCND---CL----HYYYKLK----NNTRICVSSCPPGHY---HADK 58
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IIILE OF INVENTION: Acids Encoding the Same
                                                             149 EVSEWNPWSPCTKKGKTC-GPKRGTETRVREIIOHPSAKGNLC 190
                                                                                                                                                       113 -----BRCSENXKTCTEPHXCTECR-----DGLSLQGSRC 142
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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PILING DATE: 1999-11-29
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FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOR FILING DATE: 1999-07-26
IOR APPLICATION NUMBER: US 60/146,222
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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Sao, Wei-Qiang
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CANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                      10.5%; Score 158.5; DB 4
24.9%; Pred. No. 8.5e-06;
tive 26; Mismatches 72
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30999;
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219;
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 4
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Grimaldi, Christopher J.
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Abhenazi, Avi
APPLICANT: Botstein, David
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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Search completed: June 29, 2004, 17:04:02 Job time : 15.1942 secs

246 B 246 | | 374 B 374

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Sequence 10, Appl
Sequence 34, Appl
Sequence 23, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 48, Appl
Sequence 25, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 176, Appl
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1 MHLRLISWLFIIIANFMEYIG......QQKKRKVQDKQKSVSVSTVH 272
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2: /cgm2_6/ptodata/1/pubpaa/PCT NEW FUB.pep:*
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5: /cgm2_6/ptodata/1/pubpaa/USO7_NEW FUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-894-912A-26

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4 US-10-125-852-5

0 US-09-894-912A-16

US-09-894-912A-16

US-09-894-912A-16

US-10-094-912A-16

US-10-094-912A-170-4

US-10-094-886-172

US-10-094-886-176

US-10-094-886-176
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Gapop 10.0 , Gapext 0.5
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Sequence 1779, Appl Sequence 14, Appl Sequence 18, Appl Sequence 18, Appl Sequence 25, Appl Sequence 25, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 15, Appl Sequence 17, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 21, Appl Sequence 2	20, 8, 10,
US-10-087-192-1779 US-09-894-912A-14 US-10-125-852-18 US-10-125-852-21 US-10-125-852-24 US-10-125-852-24 US-10-108-260A-4829 US-10-108-260A-4829 US-10-108-260A-4829 US-10-125-852-13 US-10-125-852-13 US-10-125-852-13 US-10-125-852-15 US-10-125-852-15 US-10-125-852-15 US-10-125-852-15 US-10-125-852-15 US-10-087-192-876 US-10-087-192-876 US-10-125-852-19	US-10-357-820-20 US-10-357-820-8 US-10-357-820-4 US-10-357-820-6 US-10-357-820-10 US-09-764-898-221
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US-09-894-912A-34
US-09-894-912A-34

Sequence 34, Application US/09894912A
Publication No. US20030044792A1
GENERAL INFORMATION:
APPLICATION ROLUSO030044792A1
TITLE OF INVENTION: PACYOR-LIKE POLYPERTIDES AND POLYNUCLEOTIDES
THE REPREMENT 2010-104-05
PRIOR PELICATION NUMBER: 00/26,614
PRIOR PELICATION NUMBER: 60/266,614
PRIOR PELICATION NUMBER: 60/215,733
PRIOR PELICATION NUMBER: 60/215,733
PRIOR PELICATION NUMBER: 09/543,774
SEQ ID NO3: 48
SOFTWARE: PATENTING DATE: 2000-04-05
SOFTWARE: 272
                                                              121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                     OHPSAKGNI, CPPTNETRKCTVORKKCOKGERGKKGRERKRKKPNKGESKEAI PDSKSLES 240
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                                        HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKRGKTCGFKRGTETRVREII 180
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                                                                                                                                                                                                                              241 SKEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
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US-10-125-852-23
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Publication No. US20030032034A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH PACTOR-:
TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-43A
CURRENT APPLICATION NUMBER: US/10/125,852
CURRENT PILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 60/316,368
PRIOR APPLICATION NUMBER: US 69/799,451
PRIOR PLING DATE: 2001-08-30
PRIOR PLING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
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US-09-894-912A-13

US-09-894-912A-13

Sequence 13, Application US/09894912A

Publication No. US20030044792A1

GENERAL INFORMATION:

APPLICANT: Tang et al.

TITE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

CURRENT APPLICANTON NUMBER: US/09/894,912A

CURRENT APPLICATION NUMBER: TO be assigned

PRIOR PILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/26,614

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-06-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

SEQ ID NOS: 48

SOFTWARE PATENTIN VERSION 3.0

SEQ ID NO 13

TYPE: PRT

CORGANISM: Homo sapiens

US-09-894-912A-13
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Best Local Similarity 100.0%; Pred. No. 5.2e-115;
Matches 272; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-852-23
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61 LFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
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181 OHPSAKGNICPPTNBTRKCTVORKKCOKGERGKKGRERKRKRPNKGESKRAIPDSKSLES 240
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Treacy, Maurice
Spaulding, Vikh
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
SPILING DATE: 18-Jun-2000
FILING DATE: 18-Jun-2000
SPILING DATE: 18-Jun-2000
STELECOMMINICATION INFORMATION:
TELECOMMINICATION 
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100.0%; Pred. No. 2.7e-112;
tive 0; Mismatches 0;
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ADDRESSER: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
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SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-745-763-166
                                                                                                                                                            241 SKEIPEORENKOOOKKRKVODKOKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                              Sequence 166, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
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STRANDEDNESS: <Unknown>
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 265; Conservative
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US-99-894-912
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                                                                                                                                                                                                                                                                                                                                                                  62 PFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLH 121
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                                                                                                                                                                                                                                                3 HIRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCAFCSDYNGCLSCKFRL
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                                                  Length 273;
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                                              ; DB 10;
1.3e-114;
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Pred. No. 2.5e-112;
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                                          Query Match 99.7%; Score 1505; DE
Best Local Similarity 100.0%; Pred. No. 1.34
Matches 271; Conservative 0; Mismatches
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US-09-894-912A-26
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PUBLICALION NO. 02-02-03-04-19-24-11

APPLICANT: Tang et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: METHODS AND POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: PACTOR-LIKE DOLGO-06-10
FRICK REPLICATION NUMBER: US/09/894,912A
CURRENT APPLICATION NUMBER: To be assigned
PRIOR PILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-06-26
PRIOR PILING DATE: 2001-06-26
PRIOR PILING DATE: 2001-01-09
SEQ ID NOS: 48
SOFTWARE: PATCHTIN VERSION 3.0
SEQ ID NOS: 48
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97.8%; Score 1477; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-112;
Matches 265; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-08-30
PRIOR PELICATION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 292
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                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-852-25
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US-10-125-652-25

US-10-125-652-25

Sequence 25, Application US/10125852

Publication No. US20030032034A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-1

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: MUMBER: US/10/125,852

CURRENT PILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: US 60/316,368
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tang et al.

APPLICANT: Tang et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
TITLE OF INVENTION: PACTOR-LIKE POLYPEPTIDES AND POLYNUCLECTIDES
FILE REPERENCE: 28110/37260A
CURRENT PEPLICATION NUMBER: US/09/894,912A
CURRENT FILING DATE: 2002-05-10
PRIOR PELICATION NUMBER: To be assigned
PRIOR PELICATION NUMBER: 60/266,614
PRIOR PELICATION NUMBER: 60/266,614
PRIOR PELICATION NUMBER: 60/215,733
PRIOR PELICATION NUMBER: 09/75,562
PRIOR PELING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 48
SOOTWARE: Retentin version 3.0
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      181 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKEA1PDSKSLES 240
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Pred. No. 2.7e-112;
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                                                                    241 SKEIPEQRENKOQOKKRKVQDKQKS 265
                                                                                                   241 SKEIPEQRENKQQQKKRKVQDKQKS 265
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                                                                                                                                                                                                                                                              Sequence 48, Application US/09894912A Publication No. US20030044792A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 265; Conservative
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US-09-894-912A-48
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Sequence 4, Application US/10185770 Publication No. US20030022217A1
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Best Local Similarity 100.
Matches 225; Conservative
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CORGANISM: Homo sapiens
US-10-185-770-4
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US-10-087-192-1782
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US-10-087-192-1782
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TITLE OF INVENTION: PACTOR-LIKE POLYBETIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: PACTOR-LIKE POLYBETIDES AND POLYNUCLEOTIDES
TILLE OF INVENTION: PACTOR-LIKE POLYBETIDES AND POLYNUCLEOTIDES
TILLE REFERENCE: 28110/37260A
CURRENT FILING DATE: 2002-05-10
FRIOR PRILING DATE: 2001-04-05
FRIOR PILING DATE: 2001-02-05
FRIOR APPLICATION NUMBER: 60/215,733
FRIOR PILING DATE: 2000-06-28
FRIOR PILING DATE: 2000-06-28
FRIOR FILING DATE: 2001-01-09
FRIOR FILING DATE: 2000-04-05
FRIOR FILING DATE: 2000-04-05
FRIOR PILING DATE: 2000-04-05
                                        61 SGYYGTRYPDINKCTKCKADCDTCPNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNHTME 120
                                                                                                                                                                              61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYL 120
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SGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNHTME 141
                                                                                                                                         CVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPPTNETRKCTV 201
                                                                                                                                                                                                                                                                                       ORIKKCOKGERGKKGRERKRKKPNKGESKBAIPDSKSLESSKEIPBORENKOQOKKRKVOD 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 KQKSVSVSTVH 251
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ORGANISM: Mus musculus
US-09-894-912A-32
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US-10-185-770-4
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GENERAL INPORMATION:
APPLICANT: CECCARDI, Toni et al.
APPLICANT: CECCARDI, Toni et al.
APPLICANT: CECCARDI, Toni et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNINEER: 60/301,852
PRIOR PILLING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASESEQ for Windows Version 4.0
SEG ID NO 4
LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDYNGCLSCKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O; Indels
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100.0%; Pred. No. 2.2e-96;
tive 0; Mismatches 0;
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLBIC ACIDS ENCODING SAME, AND METHO
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                                                                                                                                                                                                                                                                                                                                                       61 LPPALERIGAKQIGVCLSSCPSGYYGTRYPDINKCTSKCPHEKADCDTCFNKNFCTKCK 120
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                                                                                                                                                             Score 1183; DB 15; Length 239;
Pred. No. 1.9e-88;
0; Mismatches 1; Indels 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
CURRENT FILING DATE: 2002-03-07
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR APPLICATION NUMBER: 60/313,182
PRIOR APPLICATION NUMBER: 60/289,052
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Miller, Charles
Casman, Stacie
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Padigaru, Muralidhara
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Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
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Boldog, Ferenc
Guo, Xiaojia
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Best Local Similarity 97.7%;
Matches 211; Conservative
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Gerlach, Valerie
Pochart, Pascal
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Gangolli, Bsha
Gusev, Vladimir
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NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 172
LENGTH: 239
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Gorman, Linda
                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REPREEMENT: 2002-03-07
CURRENT APPLICATION NUMBER: 05/274,322
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-05-02
PRIOR PLING DATE: 2001-05-02
PRIOR PLING DATE: 2001-06-10
PRIOR PLING DATE: 2001-06-10
PRIOR PLING DATE: 2001-06-10
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-06-07
  138 HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 197
                                                                                      HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTBTRVRBII 180
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                                                                                                                                                                      181 OHPSAKGNI, CPPTNETRKCTVORKKCOKGERGKKGRERKRK 221
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; Publication No. US20040002120A1
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Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
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Fernandes, Blma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Liu, Xiaohong
Spytek, Kimberly A.
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Boldog, Perenc
Guo, Xiaojia
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Burgess, Catherine
Vernet, Corine A.
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Zerhusen, Bryan
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Gangolli, Esha
Gusev, Vladimir
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                                                                                                                                                                                                                                                                                                                              Publication No. US201
GENERAL INFORMATION:
APPLICANT: Kekuda, E
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              FRIOR APPLICATION NUMBER: 60/318,510
FRIOR APPLICATION NUMBER: 60/214,281
FRIOR APPLICATION NUMBER: 60/274,281
FRIOR APPLICATION NUMBER: 60/274,281
FRIOR APPLICATION NUMBER: 60/214,018
FRIOR PILING DATE: 2001-03-08
FRIOR FILING DATE: 2001-03-08
FRIOR PILING DATE: 2001-03-08
FRIOR PILING DATE: 2001-03-09
FRIOR PILING DATE: 2001-03-01
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Padigaru, Muralidhara
Taupier, Raymond J., Jr.
Miller, Charles
Casman, Stacie
Gaman, Stacie
Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
Gerlach, Valerie
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Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
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Liu, Xiaobong
Spytek, Kimberly A.
Patturajan, Meera
Burgess, Catherine
Vernet, Corine A.
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Gorman, Linda
Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
FILING DATE: 2001-05-02
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LENGTH: 195
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### PREPLICANT: LANDING HERRAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FIRE REPRENCE: 21402-209.
#### PILE REPRENCE: 21402-209.
### PILE REPRENCE: 2001-03-08
## PILE REPRENCE: 2001-03-08
### PILE REPRENCE: 2001-03-09
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Job time: 37.6408 secs
Pernandes, Elma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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Matches 192; Conservative
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ORGANISM: Homo sapiens
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                                                  June 29, 2004, 16:56:05; Search time 13.8641 Seconds (without alignments) 1887.186 Million cell updates/sec
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                                                                                       US-09-894-912A-34
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1 MHLRLISMLFIILNPMBYIG......QQKKRKVQDKQKSVSVSTVH 272
                                                                                                                                                                                                                                                                                                                                                                                      Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                          of hits satisfying chosen parameters:
                                                                                                                                                          283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    OM protein - protein search, using sw model
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A49128
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T27283
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B59180
C42125
CG2125
A400713
S70713
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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2: pir2:*
3: pir3:*
4: pir4:*
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4 4	12	8.3	837 1274	00	S43656 T42017	furin (BC 3.4.21.7 cysteine rich prot
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N,Alte	N'Alternate names: paired basic amino	es: pai	red bas:	֓֞֝֟֝֓֓֓֞֟֝֟֝֓֓֓֟֝֟֝֓֓֟֝֟ ֓֓֓֓֓֓֓֓֞֓֓֞֓֞֓֓֓֓֞֓֞֓֓֞֓֓֞֓֓֞֓֓֓֞	10	proprotein convertase; serin
C;Spec C;Date	C,Species: Spodoptera frugiperda C,Date: 11-Jan-2000 #sequence rev	optera 1 2000 #se	frugipe: squence	နှင့် မြ	armyworm) 11-Jan-2000 #text	change 11-Jan-2000
C; Acce	C, Accession: T43251	3251 71077				
Ricier submit A;Desc	Ricieptik, M.; Aleuk, n. submitted to the EMBL Data A;Description: Cloning and	EMBL 1	n. Data Lil and fw	ora:	nary 1996 haracterization of	FURIN from Spodoptera frugiper
A;Refe	A;Reference number: ZZ2368	per: 22;				
A; Stat	A,Accession: 143.23. A,Status: preliminary, translated	ninary;	transl	ate	d from GB/EMBL/DDBJ	
A;Mole A;Resi	A;Molecule type: mkNA A;Residues: 1-1299 <c< td=""><td>: mRNA 299 < CIB></td><td>â</td><td></td><td></td><td></td></c<>	: mRNA 299 < CIB>	â			
A; Cros	Cross-references: EMBL:Z68888; NII Experimental source: clone Sfurin	ses: EMB	BL: Z688	38; Sfu):gl167859; PID:e219690; 6; ovary	PIDN:CAA93116.1
C; Func A; Desc C; Kevw	C;Function: A;Description: responsible C;Kevwords: hvdrolase: seri	reaponsi	ible for serine	for the	ble for the endoproteolytic processing Berine proteinase	ng of proproteins with specif.
١	Cherry March		12 78.		192. DB 2. Length	1299 :
Best	geer, macen Best Local Similarity Matches 63; Conser	nilarity Conser	Vat		Pred. No. 2.7e-05; 26; Mismatches 78; Indel	81
Š	36	7SOGCOGG	3CATCSD.	ž	SCKPRLPPALERIGM	PSGYYGTRYPDINK 94
. A		CRPCAA	HCATCSE	- A	SYCRPCAAHCATCSRRADGCTSCRHHIVIADGTCWASCPPSHYBT	
ł ł			IN GOTO	Ì	THERMAL	
≩			Z-13	ģ .		:
셤	844 C	AKCHESCI	progre	ğ	CAKCHESCDÍCQGPGBIQCVICHPSIYALDGRCVISCPPAYYADKKRKBC-	GRKECMRCPVG- 899
È	153 W	NPWS PCT1	KKGKTCGI	Æ	WNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNB	TNBTRKC-TVQRKKCQK 208
đ	006	CSTCT-		İ	SAPCLSCBPKWBLNKKGKCMPVGSDKCSA	KGKCMPVGSDKCSA 933
Š	209 G	GERGKKGRERKRKKPNK	SRKRKKPI	¥.	GESKEAIPDSKSLESSKEIPE	PB 246
· 6	934	FRAVE	:: :	 TDA(GREAVDOKCKECHPACDSCYGENECHCLTCPNPNILODYKCVPE	 8 977
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334583
gerine proteinase (BC 3.4.21.-) PC6B - mouse
Grine proteinase (BC 3.4.21.-) PC6B - mouse
Grine proteinase musculus (house mouse)
Crine 102-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Crine 102-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Grine 102-1993 #sequence number 1993
Arithe: Identification of an isoform with an extremely large Cys-rich region of PC6, Areference number: S34583; MUID:93327934; PMID:8335106

RESULT 2

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furin (BC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 0.4-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C;Accession: A44434
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E. B;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E. A;Title: Cloning and functional expression of Dfurinz, a subtilisin-like proprotein prox A;Reference number: A43434; WUID:92381036; PMID:1512259
767 CVTLCPAGFYADE -- SQKNCLKCHPSCKKCVDEPEKCTVCKEGFSLARGSCIPDCEPGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-975 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: JC5570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form B-II - C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23.8ep-1997 #sequence_revision 23-8ep-1997 #text_change 20-Jun-2000
C;Accession: JC5571
R;Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na J. Biochem. 121, 941-948, 1997
A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing A;Accession: JC5571; MUD:97335942; PMID:9192737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Residues: 1-962 <MOR>
A, Residues: 1-962 <MOR>
A, Cross-references: DDBJ:DB7994; NID:g2330550; PIDN:BAA21792.1; PID:g2330551
A, Experimental Source: brain cerebellum
C, Comment: This enzyme is a processing procease and responsible for processing of variouch it is retained intracellularly.
                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 «NAK>
A;Cross-references: GB:D17583; NID:9407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        983 KTCEGNATSCNSCEGDFVLDHGVCWKTCPEKHVAVEGVCKHCPERCQDCIHEKTCKECMP 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LECNGPKEDDCKVCADTS 1091
                                                                                                                                                                                                                                                                                                                                                                        380 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPQG----TWPSYTSG 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 BVSEWNPWSPCTKKG-----KTC-----GFKRGTETRVREIIQHPSAKGNL- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 KCTKCKADCDTCFNKNPCTKCKS----GFYL4LGKCLDNCPEGLEANNHTMB-CVSIVHC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NPCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                                                                                                                                                                                                                                                                  38 SQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDI--N 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925 SCEKCSEDCVSCSGADLCQQCLSQPDNTLLLAHEGRCYHSCPEGFYAKDGVCEHCSS--PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CPPT--NETRKCTVQRKKKCQKGBRGKKGRRKKKKPNKGBSKRAIPDS
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                                                                                                                                                                                                                                                                             Gaps
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C.Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C.Keywords: glycoprotein; bydrolase; serine predicted <SIG>
F.1-62/Domain: signal sequence #status predicted <SIG>
F.19-649/Domain: bropeptide #status predicted <FRO>
F.19-649/Domain: bubtilisin homology <SET>
F.19-649/Domain: hydrophobic cluster #status predicted <HCL>
F.938-954/Domain: hydrophobic cluster #status predicted <HCL>
F.955,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F.259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                   77;
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                                                                                                                                                                                                           ch 12.4%; Score 186.5; DB 2; Length 1 Similarity 25.0%; Pred. No. 6.9e-05; 66; Conservative 31; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1092 KALHNGLCLDBCPEGTYKERENDE 1115
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A;Cross-references: GDB:131390; OMIM:167405
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   A;Accession: S34583
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C;Comment: This enzyme is a processing protease and responsible for processing of varion
ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: A novel human PACB4 isoform, PACB4B is an active processing protease containin: A;Reference number: JC5570; MUID:97335942; PMID:9192737
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                                                                                                                                                                                                                                                                                                                                                          splice form B-I
                                                                                                                                                                                                                                                                                                                                                  subtilisin-like proprotein convertase (BC 3.4.21.-) PACE4 precursor, splice form E C; Species: Homo sapiens (man)
C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JCS570
E; Manuali, A.; Manuali, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, J. Biochem. 121, 941-948, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: GDB:PACE4
A,Cross-references: GDB:131390; OMIM:167405
A,Map position: 15q26-15q26
C,Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C,Keywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
P;1-62/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: DDBJ:D87993; NID:g2330548; PIDN:BAA21791.1; PID:g2330549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- EMPGLPHKVCRRYGPPGGE-ROATVS----SKGVPG--GOSLSASSPGAGE 919
                                                                               179 IIQHPSAKGNLC----PPTNBTRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --EMPGLPHKVCRRYGPPGGE-ROATVS----SKGVPG--GOSLSASSPGAGE 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 IIQHPSAKGNLC----PPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;63-149/Domain: propeptide #status predicted <PRO>F;186-434/Domain: subtiliain homology <SBT>F;968-968/Domain: hydrophobic cluster #status predicted <HCL>F;205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 12.2%; Score 184; DB 2; Length 975; Local Similarity 26.6%; Pred. No. 7.2e-05; hes 62; Conservative 24; Mismatches 87; Indels 6
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probable proprotein convertase (BC 3.4.21.-) 5 precursor - rat

NiAlternate names: PC5 precursor
C;Species: Rattus norvegicus (Norvay rat)
C;Species: Rattus norvegicus (Norvay rat)
C;Boteis. 26-May-1994 #sequence_revision 26-May-1994 #text_change 23-Feb-1997
C;Accession: B48225
R;Lusson, J.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A;Title: cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop. A;Reference number: A48225; MUID:93342056; PMID:8341687
A;Accession: B48225
A;Status: preliminary
A;Accession: B48225
A;Status: preliminary
A;Cession: B48225
A;Status: preliminary
A;Cession: B48225
A;Cession: B4822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PACE4A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: 155527
R;Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A;Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR------ICVSSCPPGHF---H 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 PDINKCTKCKADCDTCFNKNP--CTKCKSGFYLH--LGKCLDNCPEGLEANNHTMECVSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 VHCEVSEWNPWSPCTKKGKTC-GFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSDYN--GCLSCKPRLFFALERIGMKQIGV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLFPALERIGMKQIGVCLSSCPSGYYGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Cross-references: GB:D50060; NID:g769700; PIDN:BAA08777.1; PID:g769701
C;Superfamily: subtiliisin-like proteinase PACB4; subtilisin homology
F;172-410/Domain: subtiliisin homology <BBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 168; DB 2; 26.3%; Pred. No. 0.00076; tive 25; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 167.5; DB 2 24.1%; Pred. No. 0.00083; tive 25; Mismatches 78
                                          853
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A;Accession: 152527
A;Status: preliminary; translated from GB/RMBL/DDBJ
                                      ---TCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49, Conservative
    838 FDSELIRCGECHH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 49, Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A39990
R;Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
Bya Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A;Reference number: A39490; MUD: 92075167; PMID: 1741956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1038 HLHVID-LAVCLQPCPDGYPENS----RNRTCVP-----CEPNCASCQDHPEYCTSCDMH 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------PCQEGCKTC----TSNGVCS 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCF--NKNPCTKCKSGF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 CLSSCPSGYYGTRYPDINKCTKCKADCDTCFNK-NPCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 YPGDTAARRCRR-----CHKGCETCSSRAATQCLSCR-RGFY-----HHQEMNT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780 CVTLCPAGPYADB -- SOKNCLKCHPSCKKCVDEPEKCTVCKEGPSLARGSCIPDCEPGTY 837
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 YIGSQNASRGRRQRRMHPNVSQGCQGCATCSD--YNGCLSCKPRLFFALBRIGMKQIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                                                                                                                  A;Reaidues: 1-1680 <ROB>
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-969 <KIE>
A;Cross-references: GB:M80482; NID:g189531; PIDN:AAA59998.1; PID:g189532
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A;Cross-references: GDB:131390; GMIM:167405
A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology
C;Keywords: alternative splicing; hydrolase; serine proteinase
F;150-969/Product: serine proteinase PACB4 #status predicted <SIG>
F;196-434/Domain: subtilisin homology <SBT>
F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%; Score 176.5; DB 2; Length 1680; 28.0%; Pred. No. 0.00033; vative 24; Mismatches 77; Indels 53;
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                                                                                                                                                                                                                                                                                                                    A,Cross-references: PlyBase:FBgn0004598
C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;409-652/Domain: subtiliain homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 BIIOHPSAKGNLCPPTNETRKCTVQRKK-COKGE 210
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28.8%; Pred. No. 0.00035;
tive 16; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1137 YAWQNKCLISCPDGFYADKKRLECM
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C;Species: Homo sapiens (man)
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Best Local Similarity 28.8*
Matches 44; Conservative
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Best Local Similarity
                                          A;Status: preliminary
                                                                            A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                   A; Gene: PlyBase: Fur2
A; Accession: A43434
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137 NHTMB----
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A;Accession: G02428
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-915 <MIR>
                                                                                                                     C; Accession: G02428
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C; Species Mus musculus (house mouse)
C; Species Mus musculus (house mouse)
C; Species Mus musculus (house mouse)
C; Accession: A48225; JX0248
R; Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
R; Lusson, J.; Vieau, D.; Hamelin, J.; Day, R.; Chretien, M.; Seidah, N.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 6691-6695, 1993
A.Title: CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate prop A; Reference number: A48225; MUID:93342056; PMID:8341687
A; Roccession: A48225
A; Ratus: preliminary
A; Rolling preliminary
A; Rolling Dialising Muid: A3426; PMID:323337; PIDN:AAA74636.1; PID:92933328
A; Ross references: GB:L14932; NID:9293327; PIDN:AAA74636.1; PID:92933328
A; Ross references: GB:L14932; NID:9293327; PIDN:AAA74636.1; PID:92933328
A; Ribargawa, T.; Hosaka, M.; Torii, S.; Matanabe, T.; Murakami, K.; Nakayama, K.
J. Biochem. 1135, 1392, 1993
A; Title: Identification and functional expression of a new member of the mammalian Kexz-A; Reference number: JX0248; MUID:93224489; PMID:8468318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Wolecule type: mRNA
A; Residues: 1-915 < NAK, D. 2019; NID:9220565; PIDN:BRA02143.1; PID:9220566
A; Residues: 1-915 < NAK, D. 2019; NID:9220565; PIDN:BRA02143.1; PID:9220566
A; Note: the authors translated the codon GGC for residue 915 as Ala
C; Superfamily: subtiliain-like proteinase PACE4; subtilisin homology
C; Reywords: duplication; glycoprotein; hydrolase; integrin binding; serine proteinase
F; 1-34 Domain: signal sequence #fstatus predicted < SIG>
P; 35-116/Domain: propeptide #status predicted < REO>
F; 116/Domain: subtilisin homology < SEP:
F; 164-402/Domain: subtilisin homology < SEP:
F; 173,214,388/Active site: Asp, His, Ser #status predicted
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                                                                           898
                                                 CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                                                                               ---VSIVHCEVS----EWNPWSPCTKKGKTCGFKRGTETR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSCPSGYYGTRYPDINK -- CTKCKADCDTCPNKNPCTKCKSGFYLHLGKCLDNCPEGLEA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNHTMB------NPWSPCTK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 KGKTC-----GPKR------GT---GT---BTRVREIIQHPSAKGNLCPPTNETRKCT 200
---HHQETNT 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALERIGMKQIGVCL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNSCLTCNGPGFKNCSSCPSGYLLDLGTCQMGAICKDATEESWAEGGFCMLVKKNNLC-
                                                                                                                                                                                              801 PDSBLVKCGECHHTCRTCVGPSREECIHCAKSFHPQDWKCVPACGE-----GF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                             subtilisin-like proprotein convertase (EC 3.4.21.-) PC5 precursor N;Alternate names: kexin homolog; serine proteinase PC6
-----CHKGCETCTGRSPAOCLSCR-RGFY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Indels
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                                                                                                                                                                                                                                                   176 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 167; DB 1;
; Pred. No. 0.00089;
29; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.18; 23.48;
                                                                                                                                               135 ANNHTMEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Conservative
100 YPGDAAARRCRR---
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Best Local Similarity
Matches 58; Conserva
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C;Accession: JC6148

R;Miranda, L.; Wolf, J.; Pichuantes, S.; Duke, R.; Franzusoff, A.

R;Miranda, L.; Wolf, J.; Pichuantes, S.; Duke, R.; Franzusoff, A.

Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996

A;Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1 & A;Reference number: JC6148; WUID:96353880; PMID:875538

A;Contents: CEM T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: GB:U56387; NID:g1498312; PIDN:AACS0643.1; PID:g1498313
C,Comment: This protein functions as a soluble enzyme within the secretory pathway. It
- human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GKTC-----GFKRGTE-----TRVREIIOHPSAKGNLCPPTNETRKCTV 201
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                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-899 <REU>
A;Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C;Genetics:
subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precurser - human (fr:
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNG--CLSCKPRLFFALBRIGMKQIGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 GHYHADK-KRCRKCAPN-----CESCPGSHGDQCMSCKYGYPL-----NEBINSCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C;Reywords: hydrolase; serine proteinase P;148-386/Domain: subtilisin homology <SBT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 162; DB 2; 22.3%; Pred. No. 0.0019;
                                                                                                                    R;Reudelhuber, T.L.
submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.7%; Score 162; DB
Best Local Similarity 22.3%; Pred. No. 0.001
Matches 55; Conservative 33; Mismatches
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C;Accession: 153282
R;Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.B.
Endocrinology 135, 1178-1185, 1994
A;Title: PACE4: a subtilisin-like endoprotease prevalent in the anterior pituitary and A;Reference number: 153282; MUID:94349873; PMID:8070361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 -----QCBISKCP--QPCRNGGKCIG---KSKCKCSKGYQGDLCSKPVCBPGCGAHG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | | : | | : : | : | 3.3 | 3.13 | 1.3 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3.13 | 3
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
M;Residues: 1-379 <HSI>
A;Cross-references: GB:AP122922; NID:g4585369; PIDN:AAD25402.1; PID:g4585370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene PACR4 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 CQGGCAT---CSDYNGC-------LSCKPRLFFALERIGMKQIGVCLSS----C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L31894; NID:g496221; PIDN:AAA61987.1; PID:g496222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: subtilisin-like proteinase PACB4; subtilisin homology R;177-415/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%; Score 156.5; DB 2; Length 937; 23.6%; Pred. No. 0.0044; tive 24; Mismatches 80; Indels 61;
                                                                                                                                                                                       DB 2; Length 379;
                                                                                                                                                                               ch 10.5%; Score 158.5; DB 2; Similarity 24.9%; Pred. No. 0.0017; 60; Conservative 26; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 211
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A;Molecule type: mRNA
A;Residues: 1-937 <RES>
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Best Local S
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Matches 6
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R;Hsleh, J.C.; Kodjabachian, L.; Rebbert, M.L.; Rattner, A.; Smallwood, P.M.; Samos, C.H.
Nature 398, 431-436, 1999
A;Title: A new secreted protein that binds to Wnt proteins and inhibits their activities
A;Reference number: A59180; WUID:99215557; PMID:10201374
A;Accession: A59180
SSCPSG-YYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEAN 136
                                                                                                                                                                124 THCPDGSYQDIKK---NLCRKCSENCKTCTEFHNCTECRDGLSLQGSRCSVSCEDGRYFN 780
                                                                                                                                                                                                                                                                   13.7 NHTMB-----NPWSPCTKK 162
                                                                                                                                                                                                                                                                                                             841 DISCLTCNGPGFKNCTSCPSGYLLDLGWCQMGAICKDATEESWARGGFCMLVKKNNLC-- 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 KPRLPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPRHLLIRYSLLSKEMPLKVTSTPLLYBENRVQPANNLYYLBSSISBCYCDEHC----- 225
                                                                                                                                                                                                                                                                                                                                                                                                                GKTC-----GPKRGTB------TRVRBIIQHPSAKGNLCPPTNETRKCTV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 FYLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIIOHPSAKGNLCPPTNETRKCTVQRKKCQKGBRGKKGRERKRKKPNKGESKBAIPDSKS 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein R17.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 21-Jan-2000
C;Accession: T24232
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Wnt inhibitory factor-1 - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: Z92809; PIDN: CAB07269.1; GSPDB: GN00021; CESP: R17.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 3
A;Introns: 36/3; 89/3; 179/2; 241/1; 306/1; 346/2
C;Superfamily: Caenorhabditis elegans hypothetical protein R17.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-440 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: clone R17
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Best Local S
Matches 53
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11;

61; Gaps

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F-spondin precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: You-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C; Accession: A47723
R; Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U. S.A. 90, 8268-8272, 1993
A; Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A; Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A; Reference number: A47723; MUID: 93376785; PMID: 8367492
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mANA
A; Residues: 1-803 <RUI>A; Residues: 1-803 <RUI
A; Residues: 1-804 <RUI
A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 VSQGCQGGCATCSDYNGCLSCKPRLFFALBRIGMKQIGVCLSSCPS--GYYGTRYPDINK 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.1%; Score 156; DB 2; Length 803;
Best Local Similarity 24.6%; Pred. No. 0.0042;
Matches 58; Conservative 35; Mismatches 91; Indels
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Search completed: June 29, 2004, 17:03:06 Job time: 13.8641 secs

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1 MHLRLISWLFIILNFMEYIG......QQKKRKVQDKQKSVSVSTVH 272
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                     141681 seqs, 52070155 residues
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PCKS BAACL
FURS BAACL
PCKS BAT
PCKS BAT
PCKS BAT
WIF1 HUMAN
WIF1 KNUA
PAC4 RAT
PSPO KENLA
NTC2 MOUSE
ICIR RAT
NTC2 CAT
WIF1 BAAR
ICIR RAT
WIF1 BAAR
ICIR MOUSE
FSPO RAT
WIF1 BAAR
ICIR MOUSE
ICIR MOUS
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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184.5
173.6
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168
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156.5
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140.5
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143.5
143.5
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                                                                                                         Run on:
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A Q03185 giardia lam P03185 giardia lam P03185 giardia lam P03555 sus scrofa P1683 plasmodium Q64716 rattus norv P14585 caenorhabdi P14617 drosophila Q25197 hydra atten P10411 drosophila L P10414 drosophila L P24348 caenorhabdi L	ENTS	1877 AA.		pdate)	15-MAR-2004 (Rel. 43, Last annotation update) Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21)		e 6) (SPC6).		Craniata; Vertebrata; Buteleoscomi; Sciurognathi; Muridae; Murinae; Mus.		RM PC5B).			extremely large Cys-rich region	Oregue ;				Watanabe I., Murakami K.,		sion of a new member of the	гатізу: ісв				5 X 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	tilisin/kexin-like PC5	ssed in endocrine and	(505 / 1003)	. /SEST SESS TESS 1	ATION.	., Lazure C., Nakayama K.,	4	e PCS are sorted to different					SPC7 are coexpressed with bone sites during embryogenesis.";	
VS41 GIALA TS11_GIALA TR1A_PIG TRAP_PIG TRAP TRAP_PIG TRA	ALIGNMENTS	PRT; 1	£	squence u	notation sin/kexi	(Subtilia	convertable				A. (ISOFO		5106; сауата К.	n with an	ig endoprocease		PCSA).	1218.			al expression	ng endoprotease 34.";		18 30		į		expre	1000	7699:06	ULAR LOC	Malide D		convertab	. (966)		3813:	ertson B.	and the novel protease SPC7 proteins at distinct sites	
папапапапа п		•	roato	ast se	ast an ubtil:	PC5)	cein	•	rdata entia		Z. M. MO	etine	d=833 ., Nal	Bofort	1993)		(ISOFORM PCSA)	tine; d=8463	Tori		functional	processing y to PACE4	(1993	(and Macana)		d=834	metin	nvert	•	φ. Ω	UBCEL	Z X .,	•	tein (1275 (3		N. d=869∫	Robe	vel p	֝֝֝֝֝֝֝֝֝֝֝֝֝֝֝֝֝֝֡֝֝֝֡֓֓֓֓֓֓֓֓֓֡֝
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88888777777 EETITOOOBBBB		STP	(040)	(Rel.	(Rel. convert	conver	-Inke E	Mous	Metazo a utheria	100001	330-18	TISSUE	27934; , Mura)	tion of	327:165		OM N.A.	n, and	Hosak	K.;	tion ar	Cex2-like processing similarity to PACE4	113:132-135(1993)	*	nal cor	42056;	vieau Fure of	roprote	e cells	Acad.	UENCE,	031/8; Marcin	, Seide	ne of r	1. 135;		91 KXP	Calf	, and t	2
34 126 35 125.5 36 123 37 123 39 119.5 40 119 41 119 42 118.5 44 117.5		A 1 MOUSE PCKS MOUSE	004592; 062(16-0CT-2001	15-MAR-2004 Proprotein ((Proprotein	(Subtilisin- PCSK5.	Mus musculus (Mouse)	Bukaryota; Metazoa; Chordata; Mammalia; Butheria; Rodentia;	NCBI_TaxID=1	[1] SEOUENCE OF	STRAIN=ICR;	MEDLINE=93327934; PubMed=8335106; Nakagawa T., Murakami K., Nakayama K.;	"Identificat	or PCs, a Nexz-like processing endopro FEBS Lett. 327:165-171(1993).	[2]	SEQUENCE PR(TISSUE=Brain, and Intestine, WEDLINE=91224489. DubMed=844	Nakagawa T.	Nakayama K.		mammalian Ke atructural s	J. Biochem.	[3]	TISSUE-Adrenal	MEDLINE=93342056; PubMed=8341687;	Lusson J., Vieau D., Hamelin J., Day "CDNA structure of the mouse and rat	candidate p	nonendocrine cells.";	Froc. Nati.	PARTIAL SECT	MEDLINE=9/1031/8; Fubmed=894/550; De Bie I., Marcinkiewicz M., Malide D., La	Bendayan M.	"The isoform	J. Cell Biol. 135:1261-1275(1996).	[5]	DEVELOPMENTAL EXPRESSION. MEDI.TNR=96293359: PubMed=8698813:	Constam D.B.	"SPC4, SPC6, and the no	northroderid roll
пп ппппчччч ч		£ 5.	Ų.		5 B			8	88	ŏ	25 SE	S.	X					8C 8	2 2	R.	E E	RT	꿆	R.	5 2 2	X.	5 E	RŢ	r.	Z Z	2	\$ \$	æ	RT	됩	Z.	KP V	5	8 E	Į.

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Name=PCSB; Synonyms=Long;

IsoId=Q04592-1; Sequence=Displayed;

Name=PCSA; Synonyms=Long;

IsoId=Q04592-2; Sequence=VSP 00543B, VSP 005439;

IsoSId=VSP 00543B, VSP 00543B, VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             Rancourt S.L., Rancourt D.B.; "Murine subtiliain-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation."; Dev. Genet. 21:75-81(1997).

-i- FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.
                                                                                                                                                                                                                                                                   of growth factors.

TATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Kaa-Yaa-ARG-|-Zaa bonds, where Kaa can be any amino acid and Yaa is Arg or Lys.

SUBCELLUIAL ROCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHMAY. PC5B IS A TYPE I MERBAND PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOWAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.

SIMILARITY: Belongs to peptidase family S8.
SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                          MEDLINE=97436919; PubMed=9291583;
  Cell Biol. 134:181-191(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D12619; BAA02143.1; --
EMBL; L14932; AAA74636.1; --
PIR; A48225; A48225.
PIR; S34583; S34583.
HSSP; Q99405; 1MPT.
MEROPS; S08.076; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                           DEVELOPMENTAL EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                  EARLY ENDOSOMES
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MGD; MGI:97515; Pc8k5. InterPro; IPR006212; Furin repeat. InterPro; IPR009030; Grow_Fac_recep.

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1372 DPPLYNDMCHRSCPKSPYPDMRQCVPCHKNC------LECNGPKEDDCKVCADTS 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1209 NOPCHSSCKTC---NGSLCASCPTGMYLWLQ-----ACVPSCPQG----TWPSVTSG 1253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 SQCCQGCCATCSDYNG--CLSCKPRLFFALBRIGHKQIGVCLSSCPSGYYGTRYPDI--N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCTKCKADCDTCFNKNPCTKCKS----GPYLHLGKCLDNCPBGLBANNHTMB-CVSIVHC
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ATEESWAEGGPCMLVKKNNLCQRKVLQQLCCKTCTPQG
                                                                                                                                                                                                                                                                                                    PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                          hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
Cleavage on pair of basic residues; Repeat; Alternative splicing;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC 1.

AC 2.

CLEAVAGE (AUTO-) (BY SIMILARITY).

CELLA ATTACHMENT SITE (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY

N-LINKED (GLCNAC. ) (POTENTIAL

N-LINKED (GLCNAC. .) (POTENTIAL
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MW; EC850E2DF20EALC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CYS-RICH MOTIF (CRM) REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (In isoform PC5A).
                                                                                                                                                                                                                                                                                                                         TYPE 5.
EXTRACELLULAR (POTENTIAL)
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Local Similarity 25.0%; Pred. No. 4.8e-06;
les 66; Conservative 31; Mismatches 90
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N-LINKED
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR002884; Peptidase_S8B.
InterPro; IPR002020; Protease_Inhib.
Pfam; PP00483; P_Droprocein; I.
Pfam; PR00082; Peptidase_S8; I.
PRINTS; PR00723; SUBTILISIN.
PRODOM; PD00717; P_domain; I.
PROSITE; PS00136; SUBTILASE_ASP; I.
PROSITE; PS00136; SUBTILASE_ASP; I.
PROSITE; PS00136; SUBTILASE_ASP; I.
PROSITE; PS00137; SUBTILASE_ASP; I.
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                                                                                                                                                                                                                                                                                                                                                              IsoId=09NJIS-3; Sequence=VSP 005442, VSP 005443;
-!- DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                            PCKS BRACL STANDARD; PRT; 1696 AA.

Q9NJ15; Q9NJ14; Q9NJ16;

16-OCT-2001 [Rel. 40, Created)

16-OCT-2001 [Rel. 40, Last sequence update)

28-F8B-2003 [Rel. 41, Last amortation update)

Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)

(Proprotein convertase PC6-like) (ADC6).
                                                                                                                                                                                                                       Branchiostoma californiensis (California lancelet) (Amphioxus).
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                    SEGUENCE FROM N.A. (ISOFORMS A; B AND C).
MEDLINE=20175281; PubMed=10708868;
Oliva A.A. Jr., Chan S.J., Steiner D.F.;
"Evolution of the prohormone convertases: identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=09NJ15-2; Sequence=VSP_005444, VSP_005445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bvent=Alternative splicing; Named isoforms=3;

    -!- SIMILARITY: Belongs to peptidase family S8.
    -!- SIMILARITY: Contains 1 homo B/P domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9NJ15-1; Sequence=Displayed;
InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow fac_recep.
InterPro; IPR00209; Peptidase S8.
InterPro; IPR002809; Peptidase S8.
InterPro; IPR009020; Protease inhib.
Pfam: PF01483; P_proprotein; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AP184615, AAP26300.1; -.
EMBL, AP184616; AAP26301.1; -.
EMBL, AP184617; AAP26302.1; -.
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MEROPS; S08.UPB; -.
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                                                                                                                                                                                                                                                           Branchiostoma
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                                                                             PCKS_BRACL
                                                                RESULT 2
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ------ALBRIGMKOIGVCLSSCPSGYYGTRYPDI-NKCTKCKA 100
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                                                                                                                                                                                                                                                                     DDTIIDRGECTTSCGFGEYMDRREKKCKACHPTCKECSDBY
DDTCTACNDGFLLTDASSCEAGCP -> AENQNQASFCPFA
PREVSVLABIALGHLRYSLTDVPPQSNSPPDTVLGADRARL
                                                                                                                                                                                                                                                                                                                                    Missing (In isoform C).
/FILG-WSP 005443.
/FILG-WSP 005443.
HPTCKEGSDENDUTCHACNOGFLLTDASSCEAGCPPGQFL
HHGDCDSCHRECKTC -> IARCVDRENDEWCDLVLRENPC
VRRYFVKRCCGTCKLYMEDRPMRRGSSQPTQGRN (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%; Score 184.5; DB 1; Length 1696;
22.7%; Pred. No. 6e-06;
tive 25; Mismatches 74; Indels 119; Gaps
                                                      POTENTIAL. PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                          CYS-RICH MOTIF (CRM) REGION.
CLRAVAGE (AUTO-) (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
Hydrolase, Serine protease, Glycoprotein; Zywogen, Signal;
Cleavage on pair of basic residues; Repeat; Alternative splicing;
Transmembrane.
1 25 POTENTIAL.
                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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P30432; Q24301;
01-APR-1993 [Rel. 25, Created)
10-OCT-2003 [Rel. 41, Last sequence update)
10-OCT-2003 [Rel. 42, Last annotation update)
Purin-like protease 2 precursor [BC 3.4.21.75) [Purin 2).
PURZ OR CGIST34/CG4235.
Drosophila melanogaster (Fruit £1y).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1696 AA; 188410 MW; 281CBE1784257CBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 DCDTCF--NKNPCTKCKSGFYLHLGKCLDNCPEGL------
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                                                                                                                                                                                                                                                                                                               TTATSAAGRCA (in isoform C) /FTId=VSP 005442.
                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                   CYTOPLASMIC (POTENTIAL)
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform A). / FTId=VSP 005445.
                                                                                                                                                                                                                                                                                                                                                                                                             isoform A).
/FTId=VSP 005444.
                                                                                                            POTENTIAL.
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RX GENERAL MESERCELEY B. T. For R. R. For R. R. Godayne J.D., R. Adams M.D., Celliker S. E., Holf R. N., Evans C. A., Godayne J.D., R. Adams M.D., Celliker S. E., Mile P. W., Honkins R. A., Galle R. F. Amanatides P. G., Scheers S. E., Mis P. W., Honkins R. A., Galle R. F. Godayne J. D., R. Sutchards S. Ashburner M., Henderson S. N., Sutcon G. G. Mortman J. R. Yandell M. D. Zhang Q. Chen L. X. Bardon R. C., Rogers Y. H. C., Blasel R. G. Relifer B. D., Ralley R. M. Ballew M. B. Ballewin D. B. Ballewin D. B. Develon B. D. Dew I. Dew I. Diez S. M. Durtin K. J. Bangelidan C. C. Ferriac S. Plaischmann W. Ballewin D. Houcier D. Houcier D. Gorrell J. H., Gul Z., Gunn P. Harris M. A. Ballewin D. Houcier 
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Oregon-R, Tuebingen, and Iso-1;
MTDLINE=92381035; PubMed=1512259;
MEDLINE=92381036; PubMed=1512259;
Rebbroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
"Cloning and functional expression of Dfurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with multiple
repeats of a cysteine motif;";
J. Biol. Chem. 267:17208-17215(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=180-1;
MEDLINE=9518606, PubMed=7880443;
MEDLINE=9518606, PubMed=7880443;
Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
van de Ven W.J.M.;
"The Dfurz gene of Drosophila melanogaster: genetic organization,
"The Dfurz gene of Drosophila melanogaster: genetic organization,
of its translational product Dfuring.";
DNA Cell Biol. 14:223-234(1995).
Ephydroidea, Drosophilidae, Drosophila
NCBL_TaxID=7227;
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SEQUENCE FROM N.A.
STRAIN=Berkeley;
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respective precursors. TISSUE SPECIFICITY: Transient expression in a subset of central

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nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                                                                                                                                                                                                                                    R Flydase; FBGD004558; Furz.

R GO; GO:0004276; F:furin activity; IDA.

R InterPro; IPR006121; Furin activity; IDA.

R InterPro; IPR006103; Furin repeat.

InterPro; IPR001039; Peptidase_S8.

R InterPro; IPR001039; Peptidase_S8.

InterPro; IPR001039; Peptidase_S8.

R Pfam; PF00483; P proprotein; Z.

R Pfam; PF00723; SUBTILISIN.

R ProDom; P000071; P domain; 1.

R PROSITE; PS00136; SUBTILIASE ASP; 1.

R PROSITE; PS00137; SUBTILIASE ASP; 1.

R PROSITE; PS00138; SUBTILIASE BIS; 1.

R PROSITE; PS00138; SUBTILIASE BIS; 1.

R Hydrolase; Sarine protease; Glycoprotein; Signal; Transmembrane;
                                -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
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SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILA
CHARGE RELAY SYSTEM (BY SIMILA
10 X TANDEM REPEATS, CYS-RICH.
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SIGNAL 1
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us-09-894-912a-34.rsp

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#EDLINE=97335942; PubMed=9192737;
 1087 LVMHEHK------CYSACPLDTYET---EDNKCAPCHSTCATCAGPTDQDCITCRSSR 1135
                                                                                                                                                              1037 HIHVID-LAVCLOPCPDGYPENS----RNRTCVP----CEPNCASCODHPRYCTSCDHH 1086
                         12;
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                                                 2 HLRLISWLFIILNFMEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDY-NGCLSCKPR
                                                                                                LPPALERICMKOIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCP--NKNFCTKCKSGF
                            Gaps
                                                                                                                                                                                                                                                                                PAC4 HUMAN STANDARD; PRT; 969 AA. P29122; O15099; O15100; O9UBG7; O9UBJ1; O9UBJ2; O9UBJ7; O9UBJ2; O9VBJ7; O9UBJ2; O9VBJ2; O9Y4G9; O9Y4H1; O9UBJ2; O9Y4G9; O9Y4H1; O1-DBC-1992 (Rel. 24, Created) O1-DBC-1992 (Rel. 24, Last sequence update) 15-MRA-2004 (Rel. 24, Last annotation update) Paired basic amino acid cleaving enzyme 4 precursor (RC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a second human subtilisin-like protease gene in the fess/fps region of chromosome 15."; DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Identification of novel cDNAs encoding human kexin-like protease
                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                        53;
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MEDLINB=94235049; PubMed=8179631;
Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.
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11.7%; Score 176.5; DB 1; Length 1679; 28.0%; Pred. No. 2.3e-05; ive 24; Mismatches 77; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a novel PACB4 isoform, PACB4B.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 204:1381-1382 (1994)
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TISSUE-Hepatoma, and Kidney;
MEDLINE-92075167; PubMed=1741956;
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                          60; Conservative
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 Query Match
Best Local Similarity
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constitutive secretory pathway, with unique restricted
constitutive secretory pathway, with unique restricted
distribution in both neuroendocrine and non-neuroendocrine tissues
and capable of cleavage at the RK(R)R consensus motif.

-I- CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavage of Arg-Kaa-RAG-|-Zaa bonds, where Xaa
can be any amino acid and Yaa is Arg or Lys.
-I- COPACTOR: Calcium (Potential).
-I- COPACTOR: Calcium (Potential).
-I- COPACTOR: Calcium (Potential).
-I- COPACTOR: Calcium (Potential).
-I- SUBUNIT: The PACEAA-I precursor protein seems to exist in the
reticulum endoplasmic as both a monomer, suggesting that
propeptide cleavage affects its tertiary or quaternary structure.
-I- SUBCELLUAR LOCATION: PACEAA-I and PACEAI are secreted. PACEAC
and PACEACS are not secreted and remain probably in zymogen form
in endoplasmic reticulum. PACEAR-I and PACEAB-II are retained
intracellularly probably through a hydrophobic cluster in their C-
terminus. PACEAB might be secreted.
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K., Akamatsu T., Nagamune H., Matsuda Y.; Andersu T., Nagamune H., Matsuda Y.; A novel human PACR4 isoform, PACR4B is an active processing protease containing a hydrophobic cluster at the carboxy terminus."; J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                        Tauji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
"Genomic organization and alternative splicing of human PACE4 (SPC4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
Moehring T.J.;
"Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and
can partly rescue the phenotype of a furin-deficient cell strain.";
Biochem. J. 339:639-647(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagahama M., Taniguchi T., Hashimoto B., Imamaki A., Mori K., Tsuji A., Matsuda Y.; "Biodoyntheric processing and quaternary interactions of proprotein convertase SPC4 (PACEA)."; FEBS Lett. 434:155-159(1998).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; PACE4A-II; PACE4CS; PACE4D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P29122-6; Sequence=VSP 005427, VSP_005434, VSP_005435;
Note=Probably enzymatically Inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97064242; PubMed=8906661;
Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.;
"Punctional analysis of human PACE4-A and PACE4-C isoforms:
identification of a new PACE4-CS isoform.";
PRBS Lett. 396:31-36(1996).
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Note=Probably enzymatically inactive;
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Name=PACB4A-1; Synonyms=PACB4;
IsoId=P29122-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=P29122-4; Sequence=VSP 005432, Note=Probably enzymatically inactive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=Probably enzymatically Inactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING (ISOPORM PACE4CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kexin-like processing endoprotease.";
J. Biochem. 122:438-452(1997).
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                                                                                                                                                                                                                                                                                                                PACE4E-I AND PACE4E-II).
MEDLINE=98021085; PubMed=9378725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98408849; PubMed=9738469;
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                   Name=PACEGAE-II;
Isold=P29122-8; Sequence=VSP 005436, VSP 005437;
Isold=P29122-8; Sequence=VSP 005436, VSP 005437;
Isold=P29122-8; Sequence=VSP 005436, VSP 005437;
Isold=VSR SPECIFICITY: Each PACEGA-I is expressed in heart, brain, placenta, lung, skeletal muscle, kidney, pancreas, but at comparatively higher levels in the liver. PACEA-II is at least expressed in placenta. PACEAB was only found in the embryonic kidney cell line from which it was isolated. PACEAC and PACEAD are expressed in placenta. PACEAB-II is expressed in cerebellum, placenta and pituitary. PACEAB-II is at least present in
                                                                                                                                cerebellum.
--- DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic reticulum. Isoform PACB4D lacks the propeptide domain.
--- SIMILARITY: Belongs to peptidase family $8.
--- SIMILARITY: Contains 1 homo B/P domain.
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EMBL; M80481; AAA5981;

"WBL; AB00190; BAA21620.1;

"WBL; AB001909; BAA21620.1;

J1901; BAA21620.1;

JOINED.

"A21620.1; JOINED.

"A21620.1; JOINED.

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Name=PACE4E-1;
IsoId=P29122-7; Sequence=VSP_005437;
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AB001907;
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737 YFGDTAARRCRR-----HHQEMNT 779
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Dev. Biol. 181:268-283(1997).

-I- FUNCTION: Likely to represent a widespread endoprotease activity
-i- FUNCTION: Likely to represent a widespread endoprotease activity
within the constitutive and regulated secretory pathway. Capable
of cleavage at the RX(K/R)R consensus motif. May be responsible
for the maturation of gastrointestinal peptides. May be involved
in the callular proliferation of adrenal cortex via the activation
of growth factors.
-i- CATALYTIC ACTIVITY: Release of mature proteins from their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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914403-1914;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proprotein convertase subtilisin/Kexin type 5 precursor (BC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/Kexin-like protease PC5)
(rPC5) (PC6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIATE 20214819; PubMed=10749928; Xiang Y., Molloy S.S., Thomas L., Thomas G.; Test S.C. Test Comparation of distinct trans-Golgi network/endosomal compartments."; Mol. Biol. Cell 11:1257-1273 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Zheng M., Seidah N.G., Pintex J.B.;
"The developmental expression in the rat CNS and peripheral tissues
proteases PC5 and PACE4 mRNAs: comparison with other proprotein
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De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-93342056; PubMed-8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.
"cDNa structure of the mouse and rat subtilisin/kexin-like PC5:
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                        39;
                                                                                                11.5%; Score 173.5; DB 1; Length 969; 28.8%; Pred. No. 2.2e-05; ive 16; Mismatches 54; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY
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EMBL, AB001901; BAA21624.1; JOINED.
EMBL, AB001902; BAA21624.1; JOINED.
EMBL, AB001903; BAA21624.1; JOINED.
EMBL, AB001904; BAA21624.1; JOINED.
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                                                                                                                                            44; Conservative
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                                                                                                                       Similarity
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Matches
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Event-Alternative splicing; Named isoforms=2;
Comment-Additional isoforms seem to exist;
Name=PCSB; Synonyms=Short;
Isold=P41413-1; Sequence=Displayed;
Name=PCSA; Synonyms=Short;
Isold=P41413-1; Sequence=VSP 005440, VSP 005441;
Isold=P41413-2; Sequence=VSP 005440, VSP 005441;
Isold=P41413-2; Sequence=VSP 005440, VSP 005441;
Isold=P41413-1; Sequence=VSP 005441, VSP 005441;
Isold=P61413-1; Sequence=VSP 005441, VSP 005441;
Isold=P41413-1; Sequence=VSP 005441, VSP 005441;
Isold=P41413-1; Sequence=VSP 005441, VSP 005441;
Isold=P41413-1; Sequence=VSP 005441;
Isold=P41414-1-1; Sequence=VSP 005441;
Isold=P4141-1-1; Sequence=VSP 005441;
Isold=P4141-1-1; Sequence=VSP 005441;
Isold=P4141-1-1; Sequence=VSP 005441;
Isold=P4141-1-1; Sequence=VSP 005441;
Isold=P413-1; Sequence=VSP 005441;
Isold=P413-1; Sequence=VSP 005441;
Isold=P413-1; Sequence=VSP 005441;
Isold=P413-1; Sequence=VSP 005441
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                   can be any amino acid and Yaa is Arg or Lys.
SUBCELLULAR LOCATION: PC5A IS SECREFEED THROUGH THE REGULATED
SCRETCHY PATHWAY. PC5B IS A TYPE I NEWBRANE PROTEIN LOCALIZED TO
A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
EARLY ENDOSOMES (BY SIMILARITY).
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOWAIN. AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
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R InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00209; Peptidase_S8.
R InterPro; IPR00209; Peptidase_S8.
R InterPro; IPR002010; Protecten; I.
R PRINTS; PR00723; SUBTILISIN.
R PRODOM; PD000717; P_domain; I.
R SWART; SW00261; FU; 6.
R PROSITE; PS00136; SUBTILASE_ASP; I.
R PROSITE; PS00138; SUBTILASE_SER; I.
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BY SIMILARITY.
PROPROTBIN CONVERTASB SUBTILISIN/KEXIN
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CATALYTIC.
HOMO B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: Belongs to peptidase family SB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L14933; AAA99906.1; -. EMBL; U47014; AAA87888.1; -. PIR; B48225; B48225.
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SIGNAL 1
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90 PDINKCTKCKADCDTCPNKNP--CTKCKSGPYLH--LGKCLDNCPEGLEANNHTMECVSI 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 VHCEVSEWNPWSPCTKKGKTC-GFKRGTETRVREIIQHPSAKGNLCPPTNBTRKCTVQRK 204
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MRR-2004 (Rel. 43, Last amnotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 PECSEVGCDGPGPDHCTDCLHYHYKLKNNTR------ICVSSCPPGHF---H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 PNVSQ-GCQG----GCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRY
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MRDLINE=96353880; PubMed=8755538;
Mizanda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.;
Mizanda L., Wolf D., Pichuantes S., Duke R., Franzusoff A.;
HISolation of the human PC6 gene encoding the putative host protease for HIV-1 gpl60 processing in CD4+ T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%; Score 168; DB 1; Length 1877; 26.3%; Pred. No. 0.0001; tive 25; Mismatches 54; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1877 AA; 207888 MW; 890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (In isoform PC5A). /FIId=VSP_005441.
                                                   CLEAVAGE (AUTO-) (BY CELL ATTACHMENT SITE
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SEQUENCE OF 15-913 FROM N.A.
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772 TCEDGQ 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R SMART; SM0261; FU; 5.

R PROSITE; PS61900; PLAC; 1.

DR PROSITE; PS00136; SUBTILASE ASP; 1.

DR PROSITE; PS00137; SUBTILASE HIS; 1.

DR PROSITE; PS00138; SUBTILASE SER; 1.

DR PROSITE; PS00138; SUBTILASE SER; 1.

TW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

KM Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

KM Cleavage on pair of basic residues; Repeat; Alternative splicing.

THE BY SIMILARITY.

SI 114 BY SIMILARITY.

PROPROTEIN CONVERTASE SUBTILISIN/KEXIN

THE S.
Reudelhuber T.L.;
Submitted (FRB-1996) to the EWBL/GenBank/DDBJ databases.

-!- FUNCTION: Likely to represent a widespread endoprotease activity
within the constitutive and regulated secretory pathway. Capable
of Cleavage at the RX(K/R)R consensus motif.

-!- CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavage of Arg-Xaa-Yaa-ARG-|-Zaa bonds, where Xaa
can be any maino acid and Yaa is Arg or Lys.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                 IsoId=Q92824-1; Sequence=Displayed; TISSUE SPECIFICITY: Expressed in T-lymphocytes. DOWANTS: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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R PIR; (02428); AAC50643.2; --
R PIR; (02428); G02428.
R HSSP; (039465; IMPT.
R GGENG, HGMC: 974; --
R GGONG, HGMC: 9747; PCSKS.
R MIM; 600488; --
GO; GO: 00005615; C: extracellular space; TAS.
GO; GO: 00007267; P: serine-type endopeptidase activity; TAS.
GO; GO: 00005618; P: protecolysis and peptidolysis; TAS.
InterPro; IPR00229; Peptidase S8.
InterPro; IPR00209; Peptidase S8.
InterPro; IPR00309; Protease Inhib.
R Fan; PF00483; Peptidase S8; 1.
R PRIMFS; PR00723; SUBTIAISIN.
R PRODOM; PO000777; P Gomain; 1.
R PRODOM; PO000777; P Gomain; 1.
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                                                                                                                                       Event=Alternative splicing; Named isoforms=1;
Comment=2 isoforms may be produced;
                                                                                                                                                                                                                                                     SIMILARITY: Belongs to peptidase family S8 SIMILARITY: Contains 1 homo B/P domain. SIMILARITY: Contains 1 PLAC domain.
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78; Gaps 12;
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A Itaubner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Carainar T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rockiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99215557; PubMed=10201374; M.L., Rattner A., Haieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A., Smols C.H., Nusse R., Dawid I.B., Nathans J.; An new secreted protein that binds to Wnt proteins and inhibits their activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                               78 SSCPSG-YYGTRYPDINKCTKCKADCDTCPNKNPCTKCKSGFYLHLGKCLDNCPBGLBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         779 GODCOPCHRPCATCAGAGADGCINCTEGYFMEDGRCVQSCSISYYPDHSSENGYKSCKKC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
  .) (POTENTIAL) .) (POTENTIAL)
                                                                                                                                                                                                              10.7%; Score 162; DB 1; Length 913; 22.3%; Pred. No. 0.00014; ive 33; Mismatches 81; Indels :
802 N-LINKED (GLCNAC. . .) (POTER
852 N-LINKED (GLCNAC. . .) (POTER
118 S -> F (IN REF. 3).
121 V -> A (IN REF. 3).
511 R -> A (IN REF. 3).
611 R -> Q (IN REF. 3).
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16-CCT-2001 (Rel. 40, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Wht inhibitory factor 1 precursor (WIF-1).
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 NHTMB-----
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POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 158.5; DB 1; Length 379; 24.9%; Pred. No. 0.00011; Live 26; Mismatches 72; Indels 83.
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InterPro; IPR006210; IBGF.
InterPro; IPR002010; IBGF.
InterPro; IPR002019; MIP.
InterPro; IPR002019; WIP.
InterPro; IPR002019; WIP.
InterPro; IPR00011; BGF.5.
InterPro; IPR0011; BGF.5.
IPR01115; PR00011; BGF.4.
IPR05112; PR00012; BGF.1; S.
IPR05112; PS0012; BGF.1; S.
IPR05113; PS50126; BGF.2; 4.
IPR05113; PS50126; BGF.3; S.
IPR05114; PS50126; BGF.3; S.
IPR05114; PS50126; BGF.3; S.
IPR05115; PS50126; BGF.3; S.
IPR05116; PS50126; WIP; 1.
IPR05116; PS50126; WIP; 1.
IPR051176; PS50126; WIP; 1.
IPR05117
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Q -> L (IN REF. 1).
32EC54D60529EF96 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41528 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
178
379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 605186
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16;

Gaps

83;

Conservative

Local Similarity es 60; Conserv

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                           139 IMECVSIVHCEVSEWNPWSPCTKKGKTCGPKRGTETRVREIIQHPSAKGNLCPP---- 192
                                                                                                                                                                                                                                               193 -TWETRKCTVORKKCOKGERGKKCRERKRK-----KPNKGESKEAIPDSKSLESSKEIP 245
                                                                                                                                                                                                                                                                      319 TCHEPNKC-----QCQEGWHGRHCKRYRASLIHALRPAGAQLRQHTPSLKKABERRDPP 373
                                                                                  81 PSGYYGTRYPDINKCTKC-KADCD-TCPNKNPCTKCKSGPYLHLGKCLDNCPEGLEANNH 138
  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 398:431-436 (1999).

-I- FUNCTION: Binds to WNT proteins and inhibits their activities. May be involved in mesoderm segmentation.

-I- SUBCELLULAR LOCATION: Secreted.

-I- TISSUR SPECIFICITY: During somatogenesis, expressed predominantly in unsegmented paraxial presomitic mesoderm and, to a much lesser extent, in newly segmented somites.

-I- DEVELOPMENTAL STAGE: First expressed at neurula stages.

-I- SIMILARITY: Contains 1 WIF domains.
                                                                                                              233 PPGFYG------VNCDKANCSTTCFNGGTC-----FY--PGKCI--CPPGLEGE--
                                                                                                                                                                                      41 COGGCAT---CSDYNGC------LSCKPRLFFALERIGMKQIGVCLSS----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99215557; PubMed=10201374;
HSieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,
Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;
An new secreted protein that binds to Wnt proteins and inhibits their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
128-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
WNT inhibitory factor 1 precursor (WIP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002049; Laminin EGF
InterPro; IPR003306; WIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF122924; AAD25404.1; -. HSSP; 900740; 1BDM. InterPro; IPR006209; BGF like. InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEAM; PF00008; EGF; 5.
Pfam; PF02019; WIF; 1.
PRINTS; PR00011; EGFLAMININ.
SMART; SM0181; EGF, 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PS00022; EGF_1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions on its long as its content is in no way moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       705 YPGDTAARRCRR------CHKGCEFCTGRSPTQCLSCR-RGFY-----HHQETNT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 YIGSQNASRGRRQRRMHPNVSQGCQGCCATCSDYN--GCLSCKPRLPPALERIGMKQIGV 75
                                                               pituitary and regulated by thyroid status.";
Endocrinology 135:1178-1185(1994).
-!- FUNCTION: Likely to represent an endoprotease activity within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAIRED BASIC AMINO ACID CLEAVING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Serine protease; Glycoprotein, Zymogen; Signal; Calcium; Cleavage on pair of basic residues; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ATTACHENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
"PACE4: a subtilisin-like endoprotease prevalent in the anterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 N-LINKED (GLCNAC. . .) (PO' 104053 MW; P3865557C33705C8 CRC64;
                                                                                                                                                                                                                                                                          -1- SIMILARITY: Belongs to peptidase family S8.-1- SIMILARITY: Contains 1 homo B/P domain.-1- SIMILARITY: Contains 1 PLAC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.4%; Score 156.5; DB 1
Best Local Similarity 23.6%; Pred. No. 0.00036;
Matches 51; Conservative 24; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006212; Furin repeat.
InterPro; IPR000209; Peptidase_88.
InterPro; IPR002884; Peptidase_88.
InterPro; IPR002080; Protease_Inhib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50900; PLAC; 1.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01483; P_proprotein; I.
Pfam; PF0082; Peptidase SB; 1.
PRINKS; PR0073; SUBTILISIN.
ProDom; PD000717; P domain; 1.
SMART; SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, 131894; AAA61987.1; -. PIR, 153282.
HSSP, Q99405; 1MPT.
MEROPS; S08.075; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 -----QCETSKCQ--QPCRNGGKCSG---KNKCKCSKGYQGDLCSKPVCBPSCGAHGTC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANTE-Spraque-Dawley; TISSUB-Hypothalamus, and Pituitary;
MEDLINE-94349873; PubWed-8070361;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 PPGYYGINCDKVNCTTHC-LNGGTCP-----YPGKCI--CPSGYRGB----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQGGCAT---CSDYNGC-----LSCKPRLFFALERIGMKQIGVC----LSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 PSGYYGTRYPDINKCTKCKADCDTCFNKNPCTKCKSGFYLHLGKCLDNCPEGLEANNHTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 BCVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVRBIIQHPSAKGNLCPPTNBTRKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 VQRKKCQKGERGKKGRERKRK------KPNKGESKRAIPDSKSLESSKEIPE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 IBPNKCQCKE-GWNGRYCNKKYGSNIAMALRPIGSRNRQHIPSPKRIEDRQALPE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NVV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
(Subtilisin/kexin-like protease PACB4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.4%; Score 157.5; DB 1; Length 24.3%; Pred. No. 0.00013; ive 22; Mismatches 85; Indels
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS50026; EGF_3; 4.
PROSITE; PS50814; WIF; 1.
Repeat; EGF-like domain; Signal; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LINKED (GLCNAC. . .) (PC
E26F973B0F00ACF8 CRC64;
                                                                                     POTENTIAL.
WNT INHIBITORY FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    937 AA.
                                                                                                                                  EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
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                                                                 Whit signaling pathway.
SIGNAL 29
CHAIN 29 374
DOWAIN 33 171
DOWAIN 204 235
DOWAIN 204 235
DOWAIN 268 267
                                                                                                                                                                                                          331.
181
187
195
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ઠ 셤 ઠે 요 ઠે 셤 ò 셤 Ξ

61; Gaps

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brain.
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                                                                                                                                                                                                                                                                                RESULT 11
NTC2 MOUSE
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                                                       135 ANNHTMEC-------VSIVHCEVS----EWNPWSPCTXKGKTCGFKRGTETR 175
                                                                                      853
                 CLSSCPSGYYGTRYPDINKCTKCKADCDTCPNK-NFCTKCKSGFYLHLGKCLDNCPEGLE 134
                                                                                     806 FDSELIRCGECHHTCRTCVGPSREBCIHCAKSFHFQDWKCVPACGE-----GF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;
"Scropic neural expression of a floor plate marker in frog embryos injected with the midline transcription factor Pintallavis.";
Proc. Natl. Acad. Sci. U.S.A. 90:8588-8272(1993).
-I- FUNCTION: Promotes the attachment of spinal cord and sensory neuron cells and the outgrowth of neurites in vitro. May contribute to the growth and guidance of axons in both the spinal cord and the PNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed at high levels in the floor plate.
-1- SIMILARITY: Contains 6 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F-SPONDIN.
TSP TYPR-1 1.
TSP TYPR-1 2.
TSP TYPR-1 3.
TSP TYPR-1 4.
TSP TYPR-1 5.
TSP TYPR-1 6.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·LINKED (GLCNAC. . .) (P. D3A54E329548AED9 CRC64;
                                                                                                                  176 VREIIQHPSAKGNLCPPTNETRKCTVQRKKCQKGER 211
                                                                                                                                                -----YPERMPGL--PHKVCRRCDENCLSCEGSSR 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 156; DB 1;
Pred. No. 0.00034;
                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                         803 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=93376785; PubMed=8367492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP02014; Reeler; 1.
Pfam; PP00090; tsp_1; 6.
SMART; SM00209; Tsp1; 6.
PROSITE; PS50092; Tsp1; 6.
Glycoprotein; Sigmal; Repeat; Cc
SIGNAL 1 23 POJ
                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A47723; A47723.
InterPro; IPR002861; Reeler.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L09123; AAA19105.1; -.
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                    (Rel. 29, (Rel. 29,
                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus
NCBI TaxID=8355;
                                                                                                                                                                                                                                                                                              P-spondin precursor.
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Best Local Similarity
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                                                                                                                                                                                                                                                    01-JUN-1994
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CARBOHYD
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                                                                             544 VNEECEPSSCIVTEWAEWBECS----ATCRMGMKKRHRMIKMTPADGSMCKADTTEVBK 598
                                                                                                                                                                                             138 -HTMECVSIVHCEVSEMNPWSPCTKKCKTCGFKRGTETRVREIIQHPSAKGNLCPPTNET 196
                                      37 VSQCCQGGCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPS--GYYGTRYPDINK
                                                                                                                  C--TKCK-------ADCDTCFNKNFCTKCKSGFYLHLGKCLDNCPBGLBANN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Tsujimoto Y.; in developing and adult
                                                                                                                                                                                                                                                                           197 RKCTVQRKKCQKGERGKKKGRERKRKKPNKGESKBAIPDSKSLESSKBIPEQRENKQ 252
                                                                                                                                                                                                                                                                                               MTC2 MOUSB STANDARD; PRT; 2470 AA.
035516; Q06008; Q60941;
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last sequence update)
8-FBB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRATN=CSPBL/6; TISSUE=Thymus;
ATAMAGA Y., Higuchi M., Taujimoto Y.;
"Complete amino acid sequence and mutliform transcripts encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRÓUKNCB OF 1765-2153 FROM N.A.
MEDLINE-97075110, PubMed-8917536;
Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 316-1518 FROM N.A.
SEQUENCE OF 316-1518 FROM N.A.
STRAIN-6757BL/6 X CBA; TISSUB-Embryo;
MEDLINE-93178563; PubMed-8440332;
Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of tissuses";
Exp. Cell Res. 204:364-372(1993).
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
MEDLINE-21523956; PubMed-11518718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.
Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single copy of mouse Notch2 gene.";
Submitted (UUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higuchi M., Kiyama H., Hayakawa T., Hamada Y., "Differential expression of Notch1 and Notch2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brain Res. Mol. Brain Res. 29:263-272(1995).
  35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99396706; PubMed=10393120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95333893; PubMed=7609614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development 126:3415-3424 (1999).
  58; Conservative
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InterPro; IPR002110;
  not heart.

C. !- DBVBLOPMENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.

C. !- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertage in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C. terminal fragment N(TW) and a N-terminal fragment N(BC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.

C. !- STMILARITY: Contains 35 ESF-like domains.

C. !- SIMILARITY: Contains 2 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                           WEDLINE-21374376; PubMed-11459941;
WEDLINE-21374376; PubMed-11459941;
WAIZULEAH, T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
MIZULEAH, T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
MIZULAH, T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
T. Conservation of the biochemical mechanisms of signal transduction of roces of the biochemical mechanisms of signal transduction of among mammalian Norch family members.;
T. PUNCTION: Functions as a receptor for membrane-bound ligands of Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NAIC) it forms a transcriptional activator complex with RB-J kappa and activates genes of the enhancer of split locus.

X. Affects the implementation of differentiation, proliferation and appotence in postimplementation of differentiation, proliferation and appotence of a Similarity). May play an essential role in specification and/or differentiation.

X. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2;
IsoId=035516-2; Sequence=VSP_001405;
NOte=No experimental confirmation available;
NOte=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in the brain, liver, kidney,
neuroepithelia, somites, optic vesicles and branchial arches, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein. Following proteclytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D32210; BAA22094.1; -.
EMBL; X68279; CAA48340.1; -.
EMBL; W1881; AAC52924.1; -.
BIR; A49175; A4975.
BIR; A49175; A4975.
MGD; MGI:97364; Notch2.
GO; GO:0005887; C:integral to plasma membrane; IC.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005115; P:morphogenesis of an epithelial sheet; IMP.
GO; GO:0007219; P:N signaling pathway; IC.
  Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; "Murine notch homologs (NI-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
Isold=035516-1; Sequence=Displayed;
                        proteclysis.";
J. Biol. Chem. 276:40268-40273(2001).
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bonds.
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POTENTIAL.

NUTCH EXTRACELLULAR PUNCATION.

NOTCH INTRACELLULAR DOMAIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASHIC (POTENTIAL).

ESF-LIKE 1.

ESF-LIKE 2.

ESF-LIKE 3.

ESF-LIKE 3.

ESF-LIKE 4.

ESF-LIKE 4.

ESF-LIKE 1.

ESF-LIKE 2.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 2.

ESF-LIKE 2.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 2.

ESF-LIKE 2.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 2.

ESF-LIKE 2.

ESF-LIKE 2.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 2.

ESF-LIKE 2.

ESF-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 2.

ESF-LIKE 2.

ESF-LIKE 2.

ESF-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 2.

ESF-LIKE 3.

CALCIUM-BINDING (POTENTIAL).

ESF-LIKE 3.

nterPro; IPRO01110; ANN.

InterPro; IPR001110; ANN.

InterPro; IPR001121; EGF 2.

InterPro; IPR001431; EGF 2.

InterPro; IPR001431; EGF 2.

InterPro; IPR001431; EGF 1.

InterPro; IPR00141; EGF 1.

INTERPROSITE; PR00141; EGF 1.

INTERPROSITE; EG
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EGF-LIKE 35.
LIN/NOTCH 1.
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SIMILARITY: Contains 2 fibronectin type III domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
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N-LINKED
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N-LINKED
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                                                                                                  EMBL; L29232; AAA41392.1; -.
EMBL; M27293; AAA41384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1370
                                                                                                                       HSSP; P06213; 11RK.
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  983 ENNIDECTE----SSCFNGGTCVDGINSPSCLCPVGFTGPFCLHDINECSSNPCLNAGT 1037
                                                   12;
                                                                                 QTDWNECLSEPCKNG-GTCSDYVNSYTC------TCPAGFHGVHC 982
                                                                                                                                                   125 CLDN------CPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGFKRGTETRV 176
                                                                                                            90 P-DINKCTKCKADCDTCFNKNPC-------TRCKSGPYLHLGK 124
                                                                    30 ORRMHPNVSQGCQGGCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBUNIT: TETRARER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin receptor subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                 53; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Du J., Delafontaine P.; "Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA."; Circ. Res. 76:963-972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental regulation of the rat insulin-like growth factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                             10.0%; Score 150.5; DB 1; Length 2470; 24.3%; Pred. No. 0.0024; tive 23; Mismatches 53; Indels 89;
                                                                                                                                                                                                                                                                                01-NAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor I receptor precursor (BC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE OF 913-1017 FROM N.A.
MEDLINE-92412145; PubMed=1530648;
Rurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
Rurachi H., Iche insulin receptor family, insulin receptor-related receptor, is expressed preferentially in the
                                                                                                                                                                                                       177 REIIQHPSAKGNLCPPTNETRKCTVQRKKC----QKG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989)
                                                                                                                                                                                                                                                                PRT; 1370 AA
LIN/NOTCH 2.
ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley;
MEDLINE=90017496; PubMed=2477843;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95277910; PubMed=7758167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-364 FROM N.A.
                           Query Match
Best Local Similarity 24.3%
Matches 53; Conservative
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H HSSF; PUGL19; LIKE

INTERPRO; IPR000494; EGFR L domain.

INTERPRO; IPR0004957; FW III-like.

INTERPRO; IPR000501; FW III-like.

INTERPRO; IPR000501; FW III.

INTERPRO; IPR000501; FW III.

INTERPRO; IPR000501; FW Ed recep.

INTERPRO; IPR000719; PYCH Kinase.

INTERPRO; IPR000201; RecepttyrkinsI.

INTERPRO; IPR000265; TYT pkinase.

INTERPRO; IPR000265; TYT pkinase.

INTERPRO; IPR000256; TYT pkinase.

INTERPRO; IPR000265; TYKEKINASE.

INTERPRO; IPR00069; PYKEKINASE.

INTERPRO; IPR00069; PYKEKIN II.

INTERPRO; IPR0011; PROTEIN KINASE ATP; I.

INTERPRO; IPR0011; PROTEIN KINASE DGM; I.

INTERPRO; IPR0011; PROTEIN KINASE PRO; I.

INTERPRO; IPR0011; PROTEIN KINASE PRO; I.

INTERPROPERE; PROMEIN KINASE PRO; I.

INTERPROPERE; PROMEIN KINASE PROFECT.

INTERPROPERE PROFECT.

INTERPRO
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SIGNAL 1 30 POTENTIAL.
CHAIN 31 741 INSULIN-LIKE GROWTH PACTOR I RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
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PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                               PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS00010; ASX_HYDROXYL; 23.
PROSITE; PS00022; EGF_1; 34.
PROSITE; PS00026; EGF_2; 29.
PROSITE; PS00026; EGF_3; 36.
PROSITE; PS01187; EGF_CA; 21.
Indicentiation; Neurogenesis; Repeat; ANK repeat; EGF_like domain;
Transmembrane; Signal; Glycoprotein;
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NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG.
EXTRACELLULAR (POTENTIAL).
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EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.

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EGF-LIKE 6.

EGF-LIKE 9.

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EGF-LIKE 32.

EGF-LIKE 33.

EGF-LIKE 34.

EGF-LIKE 34.

EGF-LIKE 35.

EGF-LIKE 36.

LIN/NOTCH 1.

LIN/NOTCH 1.

LIN/NOTCH 2.

LIN/NOTCH 2.

LIN/NOTCH 3.

ANK 2.

ANK 3.

ANK 4.

ANK 5.

ANK 6.
InterPro; IPR008297; Notch.
InterPro; IPR00800; Notch_dom.
Pfam; PP00023; ank; 6.
Pfam; PP00008; BGP; 36.
Pfam; PP00006; notch; 3.
PRINTS; PR001019; EGPBLOOD.
PRINTS; PR00119; EGPBLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM00179; EGE_CA; 24.
SMART; SM00179; EGE_CA; 24.
SMART; SM00179; EGE_CA; 24.
SMART; SM00179; ANK_REP_REGION; 1.
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             232 HPE----CLGSCHTPDDNTTCVACRHYYY-------KGVCVPACPPGTYRFEGMR-- 275
                                                                                                                                                                                                                                                                                                                                                     91 DINKCTKCKADCDTCFNKNFCTKC-----KSGFYLHLGKCLDNCPEGLEANN-HTMEC 142
                                                                                                                                                                                                                                                                                                                                                                              276 ------CVDRDFCANIPNAESSDSDGFVIHDGECMQECPSGFIRNSTQSMYC 321
                                                                                                                                                                                                                                                                  34 HPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYY---GTRYP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                           143 VSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSA------KGNL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 IP---CB-----GPCP---KVCG---DEBKKTKTIDSVTSAQMLQGCTILKGNL 361
                                                                                                                                                                                                                       46; Indels 66; Gaps
  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
AD -> PY (IN REP. 3).
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch protein homolog precursor (XOTCH protein)
                                                                                                                                                                         ch 9.9%; Score 149; DB 1; Length 1370; Similarity 26.7%; Pred. No. 0.0018; 47; Conservative 17; Mismatches 46; Indels 6
                                                                                                                                   MW; A5946897A41CB145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila notch.";
Science 249:1438-1441(1990).
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InterPro; IPR00110; ANK.
InterPro; IPR00115; Ask hydroxyl_S.
InterPro; IPR00142; EGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001489; EGF_II.
InterPro; IPR002049; EGF_Iike.
InterPro; IPR002049; LamInin_EGF.
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REVISIONS TO 1759-1782.
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P21783;
    CARBOHYD
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CONFLICT
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    k; Score 148.5; DB 1; Length 2524;
    t; Pred. No. 0.0035;
    32; Mismatches 102; Indels 117; Gaps

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLING-21331789; PubMed=11438922; Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.; "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain J. Comp. Neurol. 436:167-181(2001).
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28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2)
                                                                                                                                                                                                                                                                                                       MHPNVSQGCQGGCATCSDYNGCLSCKPRLFFALERIGM
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MEDLINE=93202015; PubMed=1295745;
Weinmaster G.; Roberts V.J., Lemke G.;
"Notch2: a second mammalian Notch gene.";
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28-PEB-2003 (Rel. 41, Created)
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hes 73; Conservative
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EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 4.

EGF-LIKE 8.

EGF-LIKE 9.

EGF-LIKE 10.

       EXTRACELLULAR TRUNCATION
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          CHAIN
                                                           CHAIN
          hidney.

-!- DEWELOPWENTAL STAGE: Expressed in the brain during E14 and E17.
-!- PTM: Synthesized in the endoplasmic retlculum as an inactive form which is proteolytically cleaved by a furin-like convertace in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (WEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane [P8 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
development, probably in some aspect of cell specification and/or differentiation (By similarity).

SUBSUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).

SUBSCELLULAR PLOCATION: Type I membrane protein. Following proteclytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN
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PROSITE; PS50088; ANK_REPEAT; 4.

PROSITE; PS00010; ASK_HTNOXYL; 22.

PROSITE; PS00022; EGF 1; 34.

PROSITE; PS01186; EGF 2; 26.

PROSITE; PS01187; EGF 2; 35.

PROSITE; PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; 35.

PS50026; EGF 3; EGF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Phosphorylated (By similarity).
SIMILARITY: Belongs to the NOTCH family.
SIMILARITY: Contains 35 EGF-like domains.
SIMILARITY: Contains 2 Lin/Notch repeats.
SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002110; ANK.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000181; EGF Z.
InterPro; IPR00181; EGF Z.
InterPro; IPR00181; EGF Z.
InterPro; IPR005209; EGF II.
InterPro; IPR005209; EGF II.
InterPro; IPR005209; EGF II.
InterPro; IPR008209; Notch.
InterPro; IPR00800; Notch_dom.
Pfam; PF00001; EGF 35.
Pfam; PF00001; EGF 35.
PRMP; PREPF00279; Notch; 1.
PRINTS; PR00101; EGFEMON.
PRINTS; PR0011; EGFEMON.
PRINTS; PR0011; EGFEMON.
PRINTS; PR0011; EGFEMON.
SWART; SW00128; ANK; 6.
SWART; SW00119; EGF ZA; 24.
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SIGNAL 1
CHAIN 26
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MEDLINE=20363723; PubMed=10903434;
985 ENNIDECTE----SSCFNGGTCVDGINSFSCLCPVGFTGPFCLHDINECSSNPCLNSGT 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLD-----NCPEGLEANNHTMECVSIVH-CEVSEWNPWSPCTKKGKTCGFKRGTETRV 176
                                                                                                                                                                                                                                                                                                                                                                                                 OTDWINECLSEPCKING-GTCSDYVNSYTC-------TCPAGFHGVHC 984
                                                                                                                                                                                                                                                                                                                                                                       30 QRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLPPALERIGWKQIGVCLSSCPSGYYGTRY 89
                                                                                                                                                                                                                                                                                                                                           52; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | BL14 CAEEL | STANDARD; | PRT; | 943 AA. | P51559; O44762; O44763; O44764; O44765; O44766; O1-OCT-1996 (Rel. 34, Created) | Caerbarran | A1, Created) | Caerbarran | A1, Created) | Caerbarran | A1, Caerbarran | A1, Caerbarran | Caerbarran | A2, Caerbarran | A3, Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerbarran | Caerb
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"The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/subtilisin-like endoproteases essential for early development and auth morphology.";
Genes Dev. 9:956-971(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 147.5; DB 1; Length 2471;
; Pred. No. 0.004;
23; Mismatches 52; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND FUNCTION
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QEKARPRCICPPGWDGAYCDVLNVSCKAAALQKG 1113
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MEDLINE-95293228; PubMed=7774813;
 9.88;
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Matches 54; Conserv
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MUTAGENESIS
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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R InterPro; IPR006212; Furin repeat.
R InterPro; IPR005030; Grow fac recep.
R InterPro; IPR001030; Grow fac recep.
R InterPro; IPR001030; Poptidase_S8.
R InterPro; IPR001030; Poptidase_S8.
R InterPro; IPR001031; Poptidase_S8.
R Pfam; PF001483; Poptidase_S8; I.
R PRIMTS; PR00723; SUBTILISIN.
R PROMITS; PR00171; P_domain; I.
R SMART; SR00136; SUBTILASE_ASP; I.
R PROSITE; PS00137; SUBTILASE_ASP; I.
R PROSITE; PS00137; SUBTILASE_RR; I.
R PROSITE; PS00138; SUBTILASE_RR; I.
R PROSITE; PS00138; SUBTILASE_SRR; I.
Thacker C., Srayko M., Rose A.M.;
"Mutational analysis of bli-4/kpc-4 reveals critical residues required for propriotal convertase function in C. elegans.";
Gene 252:15-25(2000).
-!- FUNCTION: The Kex2/subtilisin-like proteinase activity of this enzyme is required for the normal production of adult cuticle.
There is functional redundancy between the isoforms. Vital for embryonic and larval development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note-No experimental confirmation available:
--- TISSUE SPECIFICITY: In larvae and adults, expressed in all hypodermal cells, vulva and ventral nerve cords.
--- DEVELOPMENTAL STAGE: Expression starts at embryo two-fold stage through to adults.
--- SIMILARITY: Belongs to peptidase family SB. Furin subfamily.
--- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 651.
--- CAUTION: Ref.2 (AAB96754 and AAB96757) sequence differs from that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; SOB.031; -...
WormPep; KO4F10.4a; CE11728.
WormPep; KO4F10.4c; CE11730.
WormPep; KO4F10.4c; CE11732.
WormPep; KO4F10.4c; CE11734.
WormPep; KO4F10.4c; CE11734.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016021; F:setine-type endopeptidase activity; NAS.
GO; GO:0007592; P:cuticle biosynthesis (sensu Invertebrata); IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                           Name=D; Synonyms=d;
IsoId=P51559-1; Sequence=Displayed;
Name=A; Synonyms=a;
IsoId=P51559-2; Sequence=VSP_005416, VSP_005419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=B; Synonyms=b;
IsoId=P51559-3; Sequence=VSP_005418, VSP_005421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=C; Synonyme=c;
IsoId=P51559-4; Sequence=VSP_005422, VSP_005423;
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                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=5,
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EMBL, AR039719; AAB96754.1; ALT_SEQ.
EMBL, AR039719; AAB96755.1; --
EMBL, AR039719; AAB96756.1; --
EMBL; AR039719; AAB96757.1; ALT_SEQ.
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EMBL; L29439; AAA98751.1; ALT FRAME.
EMBL; L29440; AAA98752.1; ALT FRAME.
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Search completed: June 29, 2004, 17:00:18 Job time: 9.25243 secs

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Q968P4 018003 Q9U018 042114 076822

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042113 Q9PVZ4 O76510 Q86XX4 Q9QVW4 Q9GQ45 Q80T14

Q924Y6 Q94CB6 Q94862 Q8NCD7 Q23832 Q9B105

099KR2 Q8K2Q8

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1 MHLRLISWLFIILNFWEYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR 60
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Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
Tang R., Chen X., Wu C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Mammalla; Butheria; Primates;
NCBI_TaxID=9606;
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Matches 272; Conservat
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Q9csb2 mus musculu
Q8bvw2 mus musculu
Q9z132 mus musculu
Q9z135 homo sapien
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL 25:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listing first 45
                                                                                                                                                                                                                                     US-09-894-912A-34
1510
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Match Length
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1158
1069
644
626.5
578.5
472
472
472
472
473
192
193
176.5
176.5
                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                   Run on:
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Craniata, Vertebrata, Buteleostomi, Catarrhini, Hominidae, Homo.

ALIGNMENTS

PRT;

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0; Gaps

100.0%; Score 1510; DB 4; Length 272; 100.0%; Pred. No. 3.5e-130; ive 0, Mismatches 0; Indels 0.

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OHPSAKGNLCPPTSETRTCIVORKKCSKGERGKKGRE
241 SKRIPBORENKOOOKKRKVODKOKS 265
                                                                                              2810459H04Rik protein (Fragment).
THSD2 OR 2810459H04RIK.
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50092; TSP1; 1.
                                                        PRELIMINARY;
                                                                                                              Mus musculus (Mouse).
                                                                                                                                                     SEQUENCE PROM N.A.
                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
SEQUENCE
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                                                       09CSB2
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Q9CSB2
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                                                                181 QHPSAKGNLCPPTNETRKCTVQRKKCQKGERGKKGRERKRKKPNKGESKBAIPDSKSLES 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCFNKNFCTKCKSGFYL 120
                                                        121 HLGKCLDNCPEGLEANNHTWECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                       QHPSAKGNLCPPTNBTRKCTVQRKKCQKGERGKKGRBRKRKKPNKGBSKBAIPDSKSLBS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MHLRLISWLFIILNFWRYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OHPSAKGNLCPPTNETRKCTVQRKKCOKGERGKKGRERKRKKPNKGESKEA I PDSKSLES
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                    Hypothetical protein FLJ14440.
Momo sapiens (Human).
Bukarycia: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 96.5%; Score 1457; DB 4; Length 292; 99.2%; Pred. No. 2.7e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 292 AA; 33243 MW; 01E2774AC3D4A6F8 CRC64;
                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                      241 SKEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
                                                                                                                                241 SKEIPEQRENKQQQKKRKVQDKQKSVSVSTVH 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 263; Conservative
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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RP SEQUENCE FROM N., TASSUB-Embryo;

RX KROMING-STREALGJ; TISSUB-Embryo;

RX KARAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishij Y.,

RA Arakawa T., Jara A., Pubunishi Y., Komno H., Adachi J., Pubuda S.,

A Azawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

RA Astic T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Balalorelli R., Barsh G.,

RA Kadota K., Matsuda H.A., Ashburner M., Baldarelli R., Barsh G.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

RA Schriml L.M., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Nordone P., Ringu B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Saaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Saaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Mynshaw-Boris A., Yoshida K., Wang K.H.,

ROBI, MGI, MGI-1920030; Thad2.

RINTERPRO; IPRO0030; Grow_Fac_recep.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LPPALERICMEGIGYCLSSCPSGYYGTRYPDINKCTKCKADCDTCPNRNFCTKCKSGFYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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76.7%; Score 1158; DB 11; Length 217;
Best Local Similarity 93.1%; Pred. No. 4.5e-98;
Matches 202; Conservative 5; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AA; 24304 MW; ODCF938B9FB3FBF7 CRC64;
                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                          217 AA
241 SKEIPEGRENKOOOKKRKVODKOKS 265
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InterPro, IPR006212; Furin repeat.
InterPro, IPR009030; Grow_fac_recep.
InterPro; IPR00984; TSP1.
Pfam; PF00090; tsp. 1; 1.
SWART; SM00261; FU 2.
SWART; SM00209; TSP1; 1.
PR0SITE; PS0092; TSP1; 1.
PR0SITE; PS0092; TSP1; 1.
SROUNCE 265 AA; 29331 NW; PFRB8964743F5963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ40906.
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Interpro; IPR009030; Grow_fac_recep.
Interpro; IPR00884; TSP1.
Pfam; PR00090; tsp_1; 1.
SMART; SM00261; FU; 2.
SMART; SM00261; TSP1; 1.
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Matches 111; Conservative
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QBN7L5
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STRAIN=CSTBL/6J; TISSUB=Skin;

MEDLINE=22354683; PubMed=12466851;

The RATAN Consortium,

The RATYON Consortium,

The RATKN Genome Exploration Research Group Phase I & II Team;

The RATKN Genome Exploration Research Group Phase I & II Team;

The RATKN Genome Exploration Research Group Phase I & II Team;

The RATKN Genome Exploration Research Group Phase I & II Team;

The RATKN Genome Exploration Research Group Phase I & II Team;

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The RATKN Genome Exploration Research Group Phase I & II Team;

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The RATKN Genome Exploration Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Research Genome Factor Rese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 HLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caracta T., Katende K., Michikawa M., Yamada M., Mizusawa H.;
"R-spondin, a novel thrombospondin type 1 domain gene, expressed in the dorsal neural tube.";
Submitteed (AVG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB016768; BAA756401.; -..
MGD; MGI:2183426; Rspondin.
                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
70.8%; Score 1069; DB 11; Length 224;
Best Local Similarity 84.7%; Pred. No. 6.5e-90;
Matches 188; Conservative 9; Mismatches 25; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 OHPSAKGNLCPPTNETRKCTVQRKKCOKGERGKKGRERKRKK 222
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thrombospondin type 1 domain.
                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                    224 AA.
                                                                                                                                                                    Created)
                                                                                                                 PRT;
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                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                Thrombospondin homolog
THSD2 OR 2810459H04RIK
                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                           LERIGMKOIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNPCTKCKSGPYLHLG 123
                                                                                                                                                                                                                                                                                                                   184 SAKGNICPPINETRKCIVORKKCOKGERGKKG----RERKRKKPNKGBSKBAIPDSKSLB 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GGDHTTCSDTKBTRKCTVRRTPCPEGQKRKGGQGRRENANRHPARKNSKB--PRSNS-- 239
                                                                                                                                                                                                                                                                                                                                                                                                                124 KCLDNCPEGLEANNHTMECVSIVHCEVSEMNPWSPCTKKGKTCGFKRGTETRVREIIQHP 183
                                                                                                                                                                           Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kamehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Nakuch J., Nagai K., Isogai T.; "NEO human cDNA sequencing project."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                           5 LISWLPIILNPWBYIGSQNASRGRRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFPA
Query Match 42.6%; Score 644; DB 11; Length 265; Best Local Similarity 46.5%; Pred. No. 5.9e-51; Matches 119; Conservative 36; Mismatches 77; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Hypothetical protein.
SEQUENCE 236 AA; 25942 MW; 8D03803127EC5678 CRC64;
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SEQUENCE FROM N.A. Blakey S.;
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227 RAQB 230
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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SEQUENCE
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Q8N6X6
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the the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
for 7.0 full-length cDNAs.";

Nature 420:563-573(2002).

REMBL; AK049891; BAC33974.1; -.

REMBL; AK049891; BAC33974.1; -.

REMBL; AK049891; BAC33974.1; -.

REMBL; AK049891; BAC39891.1; -.

REMBL; AK049891; BAC39891.1; -.

REPTO; IPR006212; Purin_repeat.

InterPro; IPR006312; Purin_repeat.

InterPro; IPR00684; TSP1.

REMART; SM00209; TSP1.

REMART; SM00209; TSP1: 1.

                                                                                             92 INKCTKCKAD-CDTCFNKNFCTKCKSGFYLHLGKCLDNCPEGLEANNHTMECVSIVHCEV 150
                                                                                                                       64 MINCLIKCKIEHCEACPSHIPCTKCKEGLYLHKGRCYPACPEGSSAANGTWECSSPAQCEV 123
                                                                                                                                                                                         151 SEWNPWSPCTKKGKTCGFKRGTETRVRBIIQHPSAKGNLCPPTNETRKCTVQRKKKCQKGB 210
                                                                                                                                                                                                                     119 LHGRCFDECPDECPDGPAPLDETWECVE--GCEVGHWSEWGTCSRNRRTCGFKWGLETRTRQI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKAD-CDTCFNKNFCTKCKSGFY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 LHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 IQHPSAKGNLCPPTNETRKCTVQRKKCQKGBRGKKGRBRKRKKPNKGESKBAIPDSKSLE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHLRLISWLFIILMFWHYIGSQNASRGRRQRRMHPNVSQGCQGCATCSDYNGCLSCKPR 60
                            RMHPNVSQGCQGGCATCSDYNGCLSCKPRLPPALERIGMKQIGVCLSSCPSGYYGTRYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                    211 RGKKGRERKRKKPNKG----ESKEAIPDSKSLESSKEIPEQRENKQQQKKR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MRR-2003 (TrEMBLrel. 23, Created)
01-MRR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical thrombospondin type I repeat.
2610028F08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE-Eye, and Hippocampus; MEDLINE=22354683; PubMed=12466851; The PANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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81 RGQEVNRCKKCGATCESCFSQDFCIRCKRQFYLYKGKCLFTCPPGTLAHQWTRBCQG--E 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 CEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSAKGNLCPPTNETRKCTVQRKKCQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 REXXXQVGTGLGGUCT-GCIICSEENGCSTCQQRLFLFIRREGIRQYGXCLHDCPPGYFGI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 RRQRRMHPNVSQGCQGGCATCSDYNGCLSCKPRLFPALERIGMKQIGVCLSSCPSGYYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0000411 protein R-spondin) (Fragment).
010049416:3.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 43.3%; Pred. No. 2.7e-35;
Matches 87; Conservative 36; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Blakey S.; July 2001) to the EMBL/GenBank/DDBJ databases. Submitted (July 2001) to the EMBL/GenBank/DDBJ databases. EMBL, ALOS0325; CAB65783.3; -Genew; HGNC:16175; C20orf182.
InterPro; IPR0096312; Purin repeat.
InterPro; IPR009030; Grow_fac_recep.
InterPro; IPR009084; TSP1.
SMART; SM00261; PU; 2.
SWART; SM00261; TSP1; 1.
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC027938; AAH27938.1; -
InterPro; IPR065212; Furin repeat.
InterPro; IPR009030; Grow_fac_recep.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to putative.
Homo saplens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 A.A.
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                                                                                                                                                                                                                                           Homo sapiens (Human)
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1 MRFCLPSFALIILNCMDYSQCQ-GNRWRRNKRA-SYVSNPICKGCLSCSKDNGCSRCQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUB=Retina; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

RIAUSDER R.D., Felingold B.A., Gruse L.H., Derge J.G.,

RIAUSDER R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Bookins R.P., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Brownstein M.J., Ubdin T.B., Toshiyuki S., Carnino P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Worley N.M., Sodercia A.M., Gay L.J., Hulyk S.W.,

Raha S.S., Worley N.M., Sodercia B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Willialon D.K., Muzny D.M., Schargen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rahaesley R.M., Touchman J.M., Green B.D., Dickson M.C.,

RA Jones S.J., Marra M.A., Suallus D.E., Schnerch A., Schein J.E.,

Ray Jones S.J., Marra M.A.;

Rand mouse cDRM sequences:

Rand Mandel CDRM sequences:

Rand Mandel CDRM sequences:

Rand Mandel CDRM sequences:

Rand Mandel CDRM sequences:

Rand Mandel CDRM sequences:

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                      30.4%; Score 459.5; DB 4; Length 176; 45.1%; Pred. No. 2.9e-34; tive 30; Mismatches 53; Indels 13.
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                                                                                  176 AA; 20409 MW; 0FB3CCB1B2F8CAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 AA
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STRAIN-C57BL/6J; TISSUE-Egg;
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SMART; SM00261; FU; 1.
SMART; SM00209; TSP1; 1.
                                                                                                                                              Local Similarity 45.1%
nes 79; Conservative
                                                            PROSITE; PS50092; TSP1; 1
SEQUENCE 176 AA; 20409
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Mus musculus (Mouse).
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59 LPFPLRREGWRQYGBCLHSCPSGYYGHRAPDMNRCARCRIENCDSCPSKDFCTKCKVGFY 118
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Cieplik M., Klenk H.;
"Cloning and functional characterization of FURIN from Spodoptera
frugiperda (Sf9) cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.8%; Score 283.5; DB 11; Length llarity 42.9%; Pred. No. 2.9e-18; Conservative 24; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00261; FU; 2.
SEQUENCE 138 AA; 15172 MW; FBFD7D949279D5DD CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                  119 LHRGRCFDBCPDGPAPLDBTMBCVE--GCEVGHWS 151
                                                                                                120 LHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWN 154
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GANGION F., Jegou S., Vallarino M., Vieau D., Vaudry H.;

GANGION F., Jegou S., Vallarino M., Vieau D., Vaudry H.;

"Wolecular characterization of the cDNA and localization of the mRNA encoding the prohormone convertase PC5-A in the Buropean green frog.";

J. Comp. Neurol. 0:0-012002;

BENEL; AV131292; AAN10146.1; -6.

GO; GO:0005294; F:ATP binding; IEA.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0004389; F:electron transporter activity; IEA.

GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.

R GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron transport; IEA.

GO; GO:0006189; P:electron amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 NVSQGCQGGCATCSD-YNGCLSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease PC5-A.
Sana esculenta (Edible frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBI_TaxID=8401;
                                                                                                                                                                                                                                                                                            R GO; GO:000823); F:peptidase activity; IEA.

GO; GO:000823]; F:peptidase activity; IEA.

GO; GO:0004289; F:peptidase activity; IEA.

GO; GO:0004289; F:peptidase activity; IEA.

R InterPro; IPR00212; Furin repeat.

InterPro; IPR00212; Peptidase.SB.

InterPro; IPR00284; Peptidase.SB.

InterPro; IPR00384; Peptidase.SB.

InterPro; IPR00389; Peptidase.SB.

R InterPro; IPR00389; Peptidase.SB.

R Pfam; PP00483; P. proprotein; I.

R PRNTS; PR00723; SUBTILISIN.

R PRNAT; SW00241; FU; IO.

R PR0SITE; PS00136; SUBTILASE ASP; I.

R PROSITE; PS00136; SUBTILASE BIS; I.

R PROSITE; PS00138; SUBTILASE SIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 12.7%; Score 192; DB 5; Length 1299; Local Similarity 27.8%; Pred. No. 6.6e-09; es 63; Conservative 26; Mismatches 78; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 GERGKKGRERKRKKPNK-----GESKE---AIPDSKSLESSKEIPE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
EMBL; ZG6888; CAA93116.1; -.
HSSP; Q99405; 1MPT.
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transmembrane receptor protein tyrosine kin. . .; ISA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 GGC-ATCSDYNGC----LSCKPRLFFALERIGMKQIGVCLSSCPSGYYGTRYPDINKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheng X.J., Hughes M.A., Huston C.D., Loftus B., Gilchrist C.A., Lockhart L.A., Ghosh S., Miller-Sims V., Mann B.J., Petri M.A. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tachibana H.;

"Intermediate Subunit of the Gal/GalNAc Lectin of Entamoeba
"Intermediate Subunit of the Gal/GalNAc Lectin of Entamoeba
Bistolytica Is a Member of a Gene Family Containing Multiple CXXC
Sequence Motifs.";

Infect. Immun. 69:5892-5898(2001).

EMBL; AF337950; AAK92361.1; -..

CO, GO.0005529; F. sugar binding; IRA.

GO, GO.000157; P. heterophilic cell adhesion; IBA.

InterPro; IPR006209; EGP_like.

InterPro; IPR009309; Grow fac_recep.

PROSITE; PS01186; EGF_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%; Score 179.5; DB 13; Length 913; 29.4%; Pred. No. 6.4e-08; tive 22; Mismatches 66; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101 AA; 119512 MW; C8B6F5CBDE656ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 AA; 101864 MW; 6C9020632C47D9BB CRC64;
P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                              InterPro; IPR00045; Cytc heme B. InterPro; IPR00621; Purin_11ke. InterPro; IPR00621; Purin_repeat. InterPro; IPR006310; Grow fac_recep. InterPro; IPR006310; Grow fac_recep. InterPro; IPR006210; IEGF. InterPro; IPR00284; Peptidase_SB. InterPro; IPR00284; Peptidase_SB. InterPro; IPR009020; Protease_Inhib.
                                                                                                                                                                                                                                                                    Pfam; PF00757; Furin-like; 1.
Pfam; PF01082; Peptidaee S8; 1.
Pfam; PF01081; Pproprotein; 1.
PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P domain; 1.
SMART; SM00181; EGF; 4.
SMART; SM00261; PU; 5.
PROSITE; PS00130; CUTICHASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Bukaryota; Entamoebidae; Entamoeba.
NCBL TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=HM1:IMSS;
MEDLINE=21391855; PubMed=11500468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DBC-2001 (TrEMBLrel. 19,
01-DBC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
Gal/GalnAc lectin 1911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 29.49
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61 LPPALERIGMKQIGVCLSSCPSGYYGTRYPDINKCTKCKADCDTCF--NKNFCTKCKSGP 118
                                                                                                                          19 YLHLGKCLDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRV-R 177
                                                                                                                                                            833 YANQNKCLISCPDGFYADKKRLECM------PCQEGCKTC----TSNGVCS 873
                  734 HLHVID-LAVCLQFCPDGYFENS----RNRTCVP-----CEPNCASCQDHPEYCTSCDHH 783
                                                                                                                                                                                                  178 BIIQHPSAKGNLCPPTNETRKCTVQRKK-CQKGE 210
                                                                                                                                                                                                                                     874 ECLONWI-----LINKRDKCIVSGSEGCSESE 899
                                                                                                                                                                                                                                                                                        Search completed: June 29, 2004, 17:02:19
Job time : 35.6602 secs
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                                                        10;
                                                                                                                 89 YPDINKCTKCKADCDTCFNKNPCTK-----CKSGPYLHLGKCLDNCPEGLEA 135
                                                                                                                                                                                                                                       136 NNHTMECVSIVHCEVSEMNPWSPCTKKG-KTC--GFKRGTETRVREIIQHPSAKGNLCPP 192
                                                                                                                                                                                                                                                                         ---YPDRIKGTCIPC 932
                                                                                                                                                                                    43 GCCATCSD---YNGCL---SC----KPRLPPALE----RIGMKQIGVCLSSCPSGYYGTR 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 HIRLISWIFILLNFWEYIGSQNASRGRRQRRWHPNVSQGCQGGCATCSDY-NGCLSCKPR
                                                        Gaps
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STRAIN-Berkeley;
Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
                                                      80; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                11.7%; Score 177; DB 5; Length 1101; 26.6%; Pred. No. 1.3e-07; ative 22; Mismatches 80; Indels 5:
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PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 1376 AA; 149716 MW; B6704BAB9BABABFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
-i- SIMILARITY: COMPLINS 1 HOWO B/P DOWAIN.
EMBL; AY070553; AAL48024.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                            PRT; 1376 AA.
                                                                                                                                                                                                                                                                                                               193 TNETRKCTVQRKKCOKGERGKKGRERK 219
                                                                                                                                                                                                                                                                                                                                    FlyBase; PBGN004598; Pur2.
GO; GO:0004276; F; furin activity; IDA.
GO; GO:0004276; F; furin activity; IDA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR000512; Furin repeat.
InterPro; IPR000503; Grow fac. recep.
InterPro; IPR002894; Peptidase_S8.
InterPro; IPR002894; Peptidase_S8.
Pfam; PP00082; Peptidase_S8; 1.
PRIMTS; PR00723; SUBTILISIN.
ProDow; PD000717; P_Gomain; 1.
Query Match
Best Local Similarity 26.00,
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Q8SZS2;
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